



SEQUENCE LISTING

<110> Kato, Seishi et al.

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs  
ENCODING THESE PROTEINS

<130> GIN-6705CPUS

<140> 09/284,320

<141> 1999-04-28

<150> JP 8-301429

<151> 1996-11-13

<150> PCT/JP97/04056

<151> 1997-11-07

<160> 90

<170> PatentIn Ver. 2.0

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<211> 205

<212> PRT

<213> Homo sapiens

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Phe Arg Phe Asp Val Ala Trp Phe Leu Thr Glu Thr Ser Pro Phe Met  
35 40 45  
Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile Ser Leu Ser Val Val Gly  
50 55 60  
Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser Ser Ile Ile Gly Gly Gly  
65 70 75 80  
Val Lys Ala Pro Arg Ile Lys Thr Lys Asn Leu Val Ser Ile Ile Phe  
85 90 95  
Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile Met Ala Ile Val Ile Ser  
100 105 110  
Asn Met Ala Glu Pro Phe Ser Ala Thr Asp Pro Lys Ala Ile Gly His  
115 120 125  
Arg Asn Tyr His Ala Gly Tyr Ser Met Phe Gly Ala Gly Leu Thr Val  
130 135 140  
Gly Leu Ser Asn Leu Phe Cys Gly Val Cys Val Gly Ile Val Gly Ser  
145 150 155 160

Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro Ser Leu Phe Val Lys Ile  
165 170 175

Leu Ile Val Glu Ile Phe Gly Ser Ala Ile Gly Leu Phe Gly Val Ile  
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195 200 205

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Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln  
35 40 45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr  
50 55 60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro  
65 70 75 80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln  
85 90 95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn  
100 105 110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro  
115 120 125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn  
130 135 140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala  
145 150 155 160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr  
165 170 175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe  
180 185 190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe  
195 200 205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His

210 215 220  
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr  
225 230 235 240  
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met  
245 250 255  
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser  
260 265 270  
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val  
275 280 285  
Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg  
290 295 300  
Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe  
305 310 315 320  
Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln  
325 330 335  
Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr  
340 345 350  
Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg  
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Ala Lys Glu  
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Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro  
35 40 45  
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly  
50 55 60  
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly  
65 70 75 80  
Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His  
85 90 95

Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu  
100 105 110

Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln  
115 120 125

Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly  
130 135 140

Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro  
145 150 155 160

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His Arg Glu

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Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
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Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

Asp Cys Ser His Glu Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
305 310 315 320

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340 345

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<213> Homo sapiens

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Ala Pro Ile Cys Val Gly Ile Val Phe Leu Gly Phe Thr Pro Asp His  
35 40 45

His Cys Gln Ser Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp  
50 55 60

Ser Pro Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ala  
65 70 75 80

Gly Glu Ala Phe Leu Gly Gln Cys Arg Arg Tyr Glu Val Asp Trp Asn

85	90	95
Gln Ser Ala Leu Ser Cys Val Asp	Pro Leu Ala Ser Leu Ala Thr Asn	
100	105	110
Arg Ser His Leu Pro Leu Gly	Pro Cys Gln Asp Gly Trp Val Tyr Asp	
115	120	125
Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Ala Asp		
130	135	140
Ser Trp Lys Leu Asp Leu Phe Gln Ser Cys Leu Asn Ala Gly Phe Phe		
145	150	155 160
Phe Gly Ser Leu Gly Val Gly Tyr Phe Ala Asp Arg Phe Gly Arg Lys		
	165 170	175
Leu Cys Leu Leu Gly Thr Val Leu Val Asn Ala Val Ser Gly Val Leu		
	180 185	190
Met Ala Phe Ser Pro Asn Tyr Met Ser Met Leu Leu Phe Arg Leu Leu		
	195 200	205
Gln Gly Leu Val Ser Lys Gly Asn Trp Met Ala Gly Tyr Thr Leu Ile		
	210 215	220
Thr Glu Phe Val Gly Ser Gly Ser Arg Arg Thr Val Ala Ile Met Tyr		
	225 230	235 240
Gln Met Ala Phe Thr Val Gly Leu Val Ala Leu Thr Gly Leu Ala Tyr		
	245 250	255
Ala Leu Pro His Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro Thr		
	260 265	270
Phe Leu Phe Leu Leu Tyr Tyr Trp Cys Val Pro Glu Ser Pro Arg Trp		
	275 280	285
Leu Leu Ser Gln Lys Arg Asn Thr Glu Ala Ile Lys Ile Met Asp His		
	290 295	300
Ile Ala Gln Lys Asn Gly Lys Leu Pro Pro Ala Asp Leu Lys Met Leu		
	305 310	315 320
Ser Leu Glu Glu Asp Val Thr Glu Lys Leu Ser Pro Ser Phe Ala Asp		
	325 330	335
Leu Phe Arg Thr Pro Arg Leu Arg Lys Arg Thr Phe Ile Leu Met Tyr		
	340 345	350
Leu Trp Phe Thr Asp Ser Val Leu Tyr Gln Gly Leu Ile Leu His Met		
	355 360	365
Gly Ala Thr Ser Gly Asn Leu Tyr Leu Asp Phe Leu Tyr Ser Ala Leu		
	370 375	380
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<212> PRT
<213> Homo sapiens
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Gly Asn Trp Pro Ile Pro Gly Glu Arg Ile Pro Asp Val Ala Ala Leu
35 40 45
Ser Met Gly Phe Ser Val Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala
50 55 60
Val Gly Asn Leu Phe His Arg Pro Arg Ala Thr Val Met Val Met Val
65 70 75 80
Lys Gly Val Asn Lys Leu Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr
85 90 95

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Pro Leu Glu Asn Ala Val Pro Phe Ser Leu Asp Ser Val Ala Asn Ser  
100 105 110

Ile His Ser Leu Phe Ser Glu Glu Thr Pro Val Val Leu Gln Leu Ala  
115 120 125

Pro Ser Glu Glu Arg Val Tyr Met Val Gly Lys Ala Asn Ser Val Phe  
130 135 140

Glu Asp Leu Ser Val Thr Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln  
145 150 155 160

Glu Asn Ser Val Leu Ser Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn  
165 170 175

Asn Glu Val Asp Leu Leu Phe Leu Ser Glu Leu Gln Val Leu His Asp  
180 185 190

Ile Ser Ser Leu Leu Ser Arg His Lys His Leu Ala Lys Asp His Ser  
195 200 205

Pro Asp Leu Tyr Ser Leu Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys  
210 215 220

Arg Tyr Gly Glu Asp Ser Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu  
225 230 235 240

Val Asp Ala Leu Gln Lys Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly  
245 250 255

Gly Asn Ala Val Val Glu Leu Val Thr Val Lys Ser Phe Asp Thr Ser  
260 265 270

Leu Ile Arg Lys Thr Arg Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn  
275 280 285

Pro Ala Ser Pro Tyr Asn Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser  
290 295 300

Val Val Phe Asn Met Val Leu Trp Ile Met Ile Ala Leu Ala Leu Ala  
305 310 315 320

Val Ile Ile Thr Ser Tyr Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp  
325 330 335

Ser Ile Ile Tyr Arg Met Thr Asn Gln Lys Ile Arg Met Asp  
340 345 350

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<213> Homo sapiens

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35 40 45  
Gly Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly  
50 55 60  
Gly Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp  
65 70 75 80  
Arg Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr  
85 90 95  
Ala Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe  
100 105 110  
Val Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp  
115 120 125  
Val Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe  
130 135 140  
Lys Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn  
145 150 155 160  
Ser Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu  
165 170 175  
Phe Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Val Val  
180 185 190  
Val His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu  
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Lys

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<212> PRT  
<213> Homo sapiens

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Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro  
35 40 45  
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu

50 55 60  
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro  
65 70 75 80  
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser  
85 90 95  
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr  
100 105 110  
Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser  
115 120 125  
Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu  
130 135 140  
Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro  
145 150 155 160  
Glu Asp Glu

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<211> 92  
<212> PRT  
<213> Homo sapiens

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Thr Trp Val Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu  
20 25 30  
Ser Cys Gln Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser  
35 40 45  
Ala Gly Cys Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe  
50 55 60  
His Asp Cys Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu  
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<212> PRT  
<213> Homo sapiens

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Ala Cys Gly Met Cys Leu Gly Trp Ser Leu Arg Val Cys Phe Gly Met  
20 25 30

Leu Pro Lys Ser Lys Thr Ser Lys Thr His Thr Asp Thr Glu Ser Glu  
35 40 45

Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr Lys Met Ile Leu Val Val  
50 55 60

Arg Asn Asp Leu Lys Met Gly Lys Gly Lys Val Ala Ala Gln Cys Ser  
65 70 75 80

His Ala Ala Val Ser Ala Tyr Lys Gln Ile Gln Arg Arg Asn Pro Glu  
85 90 95

Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln Pro Lys Val Val Val Lys  
100 105 110

Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu Leu Ala His Ala Lys Met  
115 120 125

Leu Gly Leu Thr Val Ser Leu Ile Gln Asp Ala Gly Arg Thr Gln Ile  
130 135 140

Ala Pro Gly Ser Gln Thr Val Leu Gly Ile Gly Pro Gly Pro Ala Asp  
145 150 155 160

Leu Ile Asp Lys Val Thr Gly His Leu Lys Leu Tyr  
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<210> 11  
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<213> Homo sapiens

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Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln  
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Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr  
35 40 45

Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser  
50 55 60

Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn  
65 70 75 80

Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys  
85 90 95

Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr

100 105 110  
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp  
115 120 125  
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130 135 140  
Arg Lys Arg Ile His  
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Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys Gln Ser Lys  
35 40 45  
Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu Ser Ala Gly Arg Gln  
50 55 60  
Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys Leu Lys Asn Asn Asn  
65 70 75 80  
Arg Asp Leu Ser Met Val Arg Met Lys Ser Met Phe Ala Ile Gly Phe  
85 90 95  
Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser Ile Phe Asp Gly Arg  
100 105 110  
Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser Tyr Ile Gln Gly Leu  
115 120 125  
Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr Asp Cys Ser Phe Ile  
130 135 140  
Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg Gln Asn Ile Gln Lys  
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Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe Ser  
180 185

<210> 13  
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<212> PRT  
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Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys Leu Asn Glu Gln Ser  
35 40 45  
Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met Thr Phe His Tyr Ile  
50 55 60  
Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys Glu Ala Ala Phe Pro  
65 70 75 80  
Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu His Ser Glu Phe Asp  
85 90 95  
Glu Gln His Gly Lys Lys Val Pro Thr Val Ser Arg Pro Tyr Ser Phe  
100 105 110  
Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr Lys Lys Leu Tyr Ile Asp  
115 120 125  
Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile Asn Thr Glu Leu Gln Asp  
130 135 140  
Val Gln Arg Ile Met Val Ala Asn Ile Glu Glu Val Leu Gln Arg Gly  
145 150 155 160  
Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala Asn Asn Leu Ser Ser Leu  
165 170 175  
Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr Leu Asn Met Arg Ser Thr  
180 185 190  
Tyr Ala Lys Leu Ala Ala Val Ala Val Phe Phe Ile Met Leu Ile Val  
195 200 205  
Tyr Val Arg Phe Trp Trp Leu  
210 215

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20

25

30

Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala  
35 40 45  
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val  
50 55 60  
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe  
65 70 75 80  
Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser  
85 90 95  
Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His  
100 105 110

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Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu  
35 40 45  
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp  
50 55 60  
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Met  
65 70 75 80  
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly  
85 90 95  
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr  
100 105 110  
Ser Asp

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<213> Homo sapiens

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Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu Val Ile  
35 40 45  
Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu Gly Arg  
50 55 60  
Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly Arg Asn  
65 70 75 80  
Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val Glu Glu  
85 90 95  
Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu Gln Phe  
100 105 110  
Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr Thr Gly  
115 120 125  
Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val Cys Glu  
130 135 140  
Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr Lys His  
145 150 155 160  
Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile Ile Asn  
165 170 175  
Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu Ala Thr  
180 185 190  
Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met Thr Ala  
195 200 205  
Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile Ala Gln  
210 215 220  
His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile Leu Glu  
225 230 235 240  
Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His Glu Ile  
245 250 255  
Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu Ser Thr  
260 265 270  
Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val Gly Leu  
275 280 285  
Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met Asn Gln  
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Arg Met Arg Gly Leu Phe Phe  
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<210> 17  
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Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser  
20 25 30

Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys  
35 40 45

Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile  
50 55 60

Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly  
65 70 75 80

Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser Gly  
85 90 95

Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala Ile  
100 105 110

Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile Thr  
115 120 125

Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu Pro  
130 135 140

Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly Pro  
145 150 155 160

Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu Pro  
165 170 175

Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln Pro  
180 185 190

Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser Val  
195 200 205

Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met Phe  
210 215 220

Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser Thr



225	230	235	240
Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn Ile			
	245	250	255
Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro Gly			
	260	265	270
Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val Phe			
	275	280	285
Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu Thr			
	290	295	300
Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala Phe			
	305	310	315
Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly Pro			
	325	330	335
Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met Ala			
	340	345	350
Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe Leu			
	355	360	365
Phe Arg Ala Ile Val			
	370		

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<210> 18
<211> 183
<212> PRT
<213> Homo sapiens
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<400> 18  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
   1                               10                          15  
  
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
      20                      25              30  
  
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
    35                        40                45  
  
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
   50                     55               60  
  
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr  
  65                       70                 75             80  
  
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
          85                   90           95  
  
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
     100                    105              110
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Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
145 150 155 160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
165 170 175

Asp Arg His Lys Met Leu Ser  
180

<210> 19  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 19  
Met Ala Ser Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Gly  
1 5 10 15

Phe Ala Gly Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Pro Gln  
20 25 30

Val Lys Gln Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly  
35 40 45

Tyr Tyr Arg Gly Gly Phe Glu Pro Lys Met Thr Lys Arg Glu Ala Ala  
50 55 60

Leu Ile Leu Gly Val Ser Pro Thr Ala Asn Lys Gly Lys Ile Arg Asp  
65 70 75 80

Ala His Arg Arg Ile Met Leu Leu Asn His Pro Asp Lys Gly Gly Ser  
85 90 95

Pro Tyr Ile Ala Ala Lys Ile Asn Glu Ala Lys Asp Leu Leu Glu Gly  
100 105 110

Gln Ala Lys Lys  
115

<210> 20  
<211> 152  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Ala Val Leu Ser Lys Glu Tyr Gly Phe Val Leu Leu Thr Gly Ala  
1 5 10 15

Ala Ser Phe Ile Met Val Ala His Leu Ala Ile Asn Val Ser Lys Ala

20 25 30

Arg Lys Lys Tyr Lys Val Glu Tyr Pro Ile Met Tyr Ser Thr Asp Pro  
35 40 45

Glu Asn Gly His Ile Phe Asn Cys Ile Gln Arg Ala His Gln Asn Thr  
50 55 60

Leu Glu Val Tyr Pro Pro Phe Leu Phe Phe Leu Ala Val Gly Gly Val  
65 70 75 80

Tyr His Pro Arg Ile Ala Ser Gly Leu Gly Leu Ala Trp Ile Val Gly  
85 90 95

Arg Val Leu Tyr Ala Tyr Gly Tyr Tyr Thr Gly Glu Pro Ser Lys Arg  
100 105 110

Ser Arg Gly Ala Leu Gly Ser Ile Ala Leu Leu Gly Leu Val Gly Thr  
115 120 125

Thr Val Cys Ser Ala Phe Gln His Leu Gly Trp Val Lys Ser Gly Leu  
130 135 140

Gly Ser Gly Pro Lys Cys Cys His  
145 150

<210> 21  
<211> 559  
<212> PRT  
<213> Homo sapiens

<400> 21  
Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg Trp Trp Met Ala  
1 5 10 15

Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala Val Leu Leu Gly  
20 25 30

Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly Phe Tyr Ser Ser  
35 40 45

Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln Asp Glu Gln Arg  
50 55 60

Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu Asn Leu Gly Phe  
65 70 75 80

Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu Pro Leu Gly Ile  
85 90 95

Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu Val Gly Ser Ala  
100 105 110

Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala Ser Arg Asp Val  
115 120 125

Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser Leu Asn Gly Phe  
130 135 140

Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu Pro Asn Met Phe  
145 150 155 160

Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile Gly Ser Tyr Ala  
165 170 175

Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile Tyr Asp Ala Gly  
180 185 190

Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly Leu Ala Cys Leu  
195 200 205

Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu Ala Phe Pro Ala  
210 215 220

Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu Ser Gly Leu Ala  
225 230 235 240

Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr His Val Thr Thr  
245 250 255

Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu Glu Asp Gly Ser  
260 265 270

Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr Ser Glu Asn Leu  
275 280 285

Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys Ser Pro Thr Phe  
290 295 300

Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu Arg Ile Ile Phe  
305 310 315 320

Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu Val Thr Gly Gly  
325 330 335

Gln Glu His Glu Thr Asn Glu Gln Gln Gln Lys Val Ala Glu Thr Val  
340 345 350

Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu Leu Cys Leu Leu  
355 360 365

Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg Ile Lys Asp Cys  
370 375 380

Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp Ala Arg Asp Gly  
385 390 395 400

Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys Ile Gln Lys Leu  
405 410 415

Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu Leu Leu Val Gly  
420 425 430

Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu Gln Phe Val Thr  
435 440 445

Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His Ser Ala Cys Gly  
450 455 460

Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe Gly Thr Leu Thr  
465 470 475 480

Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu Leu Gln Gln Pro  
485 490 495

Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu Pro Phe Trp Val  
500 505 510

Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe Leu Leu Pro Ser  
515 520 525

Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu Tyr Ala Ala Asn  
530 535 540

Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu Val Thr Ala  
545 550 555

<210> 22  
<211> 330  
<212> PRT  
<213> Homo sapiens

<400> 22  
Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu Leu Phe  
1 5 10 15

Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro Glu Pro  
20 25 30

Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile Asn Val Thr  
35 40 45

Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val Val Leu Asn  
50 55 60

Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu Pro Val Asn  
65 70 75 80

Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val Lys Asn Glu  
85 90 95

Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile Val Ser Val  
100 105 110

Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser Ser Leu Gln  
115 120 125

Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly Lys Gln Val  
130 135 140

Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys Asn Arg Gly  
145 150 155 160  
Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu  
165 170 175  
Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu  
180 185 190  
Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu  
195 200 205  
Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys  
210 215 220  
Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val  
225 230 235 240  
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe Trp  
245 250 255  
Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met Val Val  
260 265 270  
Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys Val Phe Phe  
275 280 285  
Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys Val Asp Val  
290 295 300  
Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro Glu Lys Arg  
305 310 315 320  
Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile  
325 330

<210> 23  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 23  
Met Ser Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala  
1 5 10 15  
Val Thr Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys  
20 25 30  
Arg Phe Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His  
35 40 45  
Ile Gln Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp  
50 55 60  
Leu Gly Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe

[illegible]

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<210> 24
<211> 101
<212> PRT
<213> Homo sapiens
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```
<400> 24  
Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg  
1                    5              10             15  
  
Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val  
                20              25             30  
  
Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr  
        35              40             45  
  
Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe  
    50              55             60  
  
Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile  
   65              70             75             80  
  
Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Il  
          85              90             95  
  
Pro Leu Gly Thr Pro  
            100
```

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<210> 25
<211> 372
<212> PRT
<213> Homo sapiens
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<400> 25
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
  1                               10                      15
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
      20                               25                      30
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
      35                               40                      45
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
      50                               55                      60
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
      65                               70                      75                      80

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Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln  
85 90 95

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Val  
100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg  
115 120 125

Thr Trp Gly Arg Glu Arg Lys Val Arg Gly Leu Gln Leu Arg Leu Leu  
130 135 140

Phe Leu Val Gly Thr Ala Ser Asn Pro His Glu Ala Arg Lys Val Asn  
145 150 155 160

Arg Leu Leu Glu Leu Glu Ala Gln Thr His Gly Asp Ile Leu Gln Trp  
165 170 175

Asp Phe His Asp Ser Phe Phe Asn Leu Thr Leu Lys Gln Val Leu Phe  
180 185 190

Leu Gln Trp Gln Glu Thr Arg Cys Ala Asn Ala Ser Phe Val Leu Asn  
195 200 205

Gly Asp Asp Asp Val Phe Ala His Thr Asp Asn Met Val Phe Tyr Leu  
210 215 220

Gln Asp His Asp Pro Gly Arg His Leu Phe Val Gly Gln Leu Ile Gln  
225 230 235 240

Asn Val Gly Pro Ile Arg Ala Phe Trp Ser Lys Tyr Tyr Val Pro Glu  
245 250 255

Val Val Thr Gln Asn Glu Arg Tyr Pro Pro Tyr Cys Gly Gly Gly Gly  
260 265 270

Phe Leu Leu Ser Arg Phe Thr Ala Ala Ala Leu Arg Arg Ala Ala His  
275 280 285

Val Leu Asp Ile Phe Pro Ile Asp Asp Val Phe Leu Gly Met Cys Leu  
290 295 300

Glu Leu Glu Gly Leu Lys Pro Ala Ser His Ser Gly Ile Arg Thr Ser  
305 310 315 320

Gly Val Arg Ala Pro Ser Gln His Leu Ser Ser Phe Asp Pro Cys Phe  
325 330 335

Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu  
340 345 350

Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln  
355 360 365

Thr Gln Ile Tyr  
370



<210> 26  
<211> 615  
<212> DNA  
<213> Homo sapiens

<400> 26  
atgacggggc tagcactgct ctactccggg gtcttcgtgg ccttctgggc ctgcgcgctg 60  
gccgtgggag tctgctacac catttttgat ttgggcttcc gctttgatgt ggcatgggtc 120  
ctgacggaga cttcgccctt catgtggtcc aacctgggca ttggcctagc tatctccctg 180  
tctgtgggtg gggcagcctg gggcatctat attaccggt cctccatcat tggaggagga 240  
gtgaaggccc ccaggatcaa gaccaagaac ctggtcagca tcatcttctg tgaggctgtg 300  
gccatctacg gcatcatcat ggcaattgtc attagcaaca tggtgagcc ttccagtgcc 360  
acagacccca aggccatcgg ccacggaac taccatgcag gctactccat gtttggggct 420  
ggcctcaccg taggcctgtc taacctcttc tgtggagtct gcgtgggcat cgtgggcagt 480  
ggggctgccc tggccgatgc tcagaacccc agcctctttg taaagattct catcgtggag 540  
atctttggca gcgccattgg cctctttggg gtcacgtcg caattcttca gacctccaga 600  
gtgaagatgg gtgac 615

<210> 27  
<211> 1113  
<212> DNA  
<213> Homo sapiens

<400> 27  
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tatccggggg ggccccagcc acccatgccc cctatgctc agcctcccta cctgggggcc 120  
ccttaccac agccccctt ccagccctcc cctacggtc agccagggtta ccccatggc 180  
cccagccct accccaagg gggctaccca cagggtccct accccaagg gggctaccca 240  
caggggccct accacaaga gggctaccca caggggccct accccaagg gggctacccc 300  
caggggccat atccccagag ccccttcccc cccaaccct atggacagcc acaggtcttc 360  
ccaggacaag accctgactc accccagcat ggaaactacc aggaggaggg tccccatcc 420  
tactatgaca accaggactt cctgccacc aactgggatg acaagagcat ccgacaggcc 480  
ttcatccgca aggtgttcct agtgetgacc ttgcagctgt cggtgaccct gtccacgggtg 540  
tctgtgttca cttttgttgc ggaggtgaag ggctttgtcc gggagaatgt ctggacctac 600

tatgtctcct atgctgtctt cttcatctct ctcacgtcc tcagctgttg tggggacttc 660  
cggcgaaagc acccctggaa ccttggtgca ctgtcgggtcc tgaccgccag cctgtcgtac 720  
atggtgggga tgatcgccag cttctacaac accgagcgag tcatcatggc cgtgggcac 780  
accacagccg tctgcttcac cgtcgtcatc ttctccatgc agaccgcga cgacttcacc 840  
tcatgcatgg gcgtgctcct ggtgagcatg gtggtgctct tcatcttcgc cattctctgc 900  
atcttcatcc ggaaccgcat cctggagatc gtgtacgcct cactgggcgc tctgctcttc 960  
acctgcttcc tcgcagtga caccagctg ctgctgggga acaagcagct gtcctgagc 1020  
ccagaagagt atgtgtttgc tgcgctgaac ctgtacacag acatcatcaa catcttcctg 1080  
tacatcctca ccatcattgg ccgcgccaaag gag 1113

<210> 28  
<211> 537  
<212> DNA  
<213> Homo sapiens

<400> 28  
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caagtcctaa attttgaat gattgtctca tcggcactaa tgatctggaa ggggttaatg 120  
gtaataactg gaagtgaag tccgattgta gtggtgctca gtggcagcat ggaacctgca 180  
tttcatagag gagatcttct ctttctaaca aatcgagttg aagatcccat acgagtggga 240  
gaaattgttg tttttaggat agaaggaaga gagattccta tagttcaccg agtcttgaag 300  
attcatgaaa agcaaatgg gcatatcaag tttttgacca aaggagataa taatgcggtt 360  
gatgaccgag gcctctataa acaaggacaa cattggctag agaaaaaaga tgttgtgggg 420  
agagccaggg gatgtgttcc ttatattgga attgtgacga tcctcatgaa tgactatcct 480  
aaatttaagt atgcagttct ctttttgctg ggtttattcg tgctggttca tcgtgag 537

<210> 29  
<211> 1041  
<212> DNA  
<213> Homo sapiens

<400> 29  
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ccatctggag tgcggctggt ggggggcctc caccgctgtg aaggcggggt ggaggtggaa 120  
cagaaaggcc agtggggcac cgtgtgtgat gacggctggg acattaagga cgtggctgtg 180  
ttgtgccggg agctgggctg tggagctgcc agcggaaccc ctagtggtat ttgtatgag 240

ccaccagcag aaaaagagca aaaggtcctc atccaatcag tcagttgcac aggaacagaa 300  
gatacattgg ctcaagtgtga gcaagaagaa gtttatgatt gttcacatga agaagatgct 360  
ggggcatcgt gtgagaacct agagagctct ttctccccag tcccagaggg tgtcaggctg 420  
gctgacggcc ctgggcattg caagggacgc gtggaagtga agcaccagaa ccagtgggtat 480  
accgtgtgcc agacaggctg gagcctccgg gccgcaaagg tgggtgtgccg gcagctggga 540  
tgtgggaggg ctgtactgac tcaaaaacgc tgcaacaagc atgcctatgg ccgaaaacct 600  
atctggctga gccagatgtc atgctcagga cgagaagcaa cccttcagga ttgcccttct 660  
gggccttggg ggaagaacac ctgcaacct gatgaagaca cgtgggtcga atgtgaagat 720  
ccctttgact tgagactagt aggaggagac aacctctgct ctgggcgact ggaggtgctg 780  
cacaagggcg tatggggctc tgtctgtgat gacaactggg gagaaaagga ggaccagggtg 840  
gtatgcaagc aactgggctg tgggaagtcc ctctctccct ccttcagaga ccggaaatgc 900  
tatggccctg gggttggccg catctggctg gataatgttc gttgctcagg ggaggagcag 960  
tccctggagc agtgccagca cagattttgg gggtttcacg actgcacca ccaggaagat 1020  
gtggctgtca tctgctcagg a 1041

<210> 30  
<211> 1662  
<212> DNA  
<213> Homo sapiens

<400> 30  
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ttcctgggtt tcacacctga ccaccactgc cagagtcctg ggggtggtga gctgagccag 180  
cgctgtggct ggagccctgc ggaggagctg aactatacag tgccaggcct ggggcccgcg 240  
ggcgaggcct tccttggcca gtgcaggcgc tatgaagtgg actggaacca gagcgccctc 300  
agctgtgtag acccctggc tagcctggcc accaacagga gccacctgcc gctgggtccc 360  
tgccaggatg gctgggtgta tgacacgcc ggctcttcca tcgtactga gttcaacctg 420  
gtgtgtgctg actcctggaa gctggacctc tttcagtcct gtttgaatgc gggcttcttc 480  
tttggtcttc tcgggtgttg ctactttgca gacaggttt gccgtaagct gtgtctcctg 540  
ggaactgtgc tggtaacgc ggtgtcgggc gtgctcatgg ccttctcgcc caactacatg 600  
tccatgctgc tcttccgcct gctgcagggc ctggtcagca agggcaactg gatggctggc 660

tacaccctaa tcacagaatt tgttggctcg ggctccagaa gaacggtggc gatcatgtac 720  
cagatggcct tcacggtggg gctggtggcg cttaccgggc tggcctacgc cctgcctcac 780  
tggcgctggc tgcagctggc agtctccctg cccaccttcc tcttctgct ctactactgg 840  
tgtgtgccgg agtccccctg gtggctgtta tcacaaaaaa gaaacactga agcaataaag 900  
ataatggacc acatcgctca aaagaatggg aagttgcctc ctgctgattt aaagatgctt 960  
tccctcgaag aggatgtcac cgaaaagctg agcccttcat ttgcagacct gttccgcacg 1020  
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tatcaggggc tcactctgca catggggccc accagcggga acctctacct ggatttcctt 1140  
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ggcgcgatct accccatggc cgtgtcaaatt ttgttggcgg gggcagcctg cctcgtcatg 1260  
atttttatct cacctgacct gcactgggta aacatcataa tcattgtgtg tggccgaatg 1320  
ggaatcacca ttgcaatata aatgatctgc ctggtgaatg ctgagctgta cccacattc 1380  
gtcaggaacc tcggagtgat ggtgtgttcc tcctgtgtg acataggtgg gataatcacc 1440  
cccttcatag tcttcaggct gagggaggtc tggcaagcct tgccccctcat tttgtttgcg 1500  
gtgttggggc tgcttgccgc gggagtgcag ctacttcttc cagagaccaa gggggtcgct 1560  
ttgccagaga ccatgaagga cgccgagaac cttgggagaa aagcaaagcc caaagaaaac 1620  
acgatttacc ttaaggtcca aacctcagaa ccctcgggca cc 1662

<210> 31  
<211> 1050  
<212> DNA  
<213> Homo sapiens

<400> 31  
atggctgtgt ttgtcgtgct cctggcggtg gtggcgggtg ttttggggaa cgagtttagt 60  
atattaaaat caccagggtc tgttggtttc cgaaatggaa attggcctat accaggagag 120  
cggatcccag acgtggctgc attgtccatg ggcttctctg tgaaagaaga ctttcttgg 180  
ccaggactcg cagtgggtaa cctgtttcat cgtcctcggg ctaccgtcat ggtgatggtg 240  
aagggagtga acaaactggc tctaccccca ggcagtgtca tttcgtacct tttggagaat 300  
gcagttcctt ttagtcttga cagtgttgca aattccattc actccttatt ttctgaggaa 360  
actcctgttg ttttgcagtt ggctcccagt gaggaaagag tgtatatggt agggaaggca 420  
aactcagtgt ttgaagacct ttcagtcacc ttgcgccagc tccgtaatcg cctgtttcaa 480

gaaaactctg ttctcagttc actccccctc aattctctga gtaggaacaa tgaagttgac 540  
ctgctctttc tttctgaact gcaagtgtca catgatattt caagcttgct gtctcgatcat 600  
aagcatctag ccaaggatca ttctcctgat ttatattcac tggagctggc aggtttggat 660  
gaaattggga agcgttatgg ggaagactct gaacaattca gagatgcttc taagatcctt 720  
gttgacgtc tgcaaaagtt tgcagatgac atgtacagtc tttatgggtg gaatgcagt 780  
gtagagttag tcaactgtcaa gtcatttgac acctccctca ttaggaagac aaggactatc 840  
cttgaggcaa aacaagcgaa gaaccagca agtccctata accttgcata taagtataat 900  
tttgaatatt ccgtggtttt caacatggta ctttggataa tgatgcctt ggccttggct 960  
gtgattatca cctcttaca tatttggaa atggatcctg gatatgatag catcatttat 1020  
aggatgacaa accagaagat tcgaatggat 1050

<210> 32  
<211> 627  
<212> DNA  
<213> Homo sapiens

<400> 32  
atgggtgtcct ctccctgcac gcaggcaagc tcacggattt gctcccgat cctgggactg 60  
agccttggga ctgcagccct gtttctgtgt ggggccaacg tggcactcct ccttcctaac 120  
tgggatgtca cctacctgtt gaggggcctc cttggcaggc atgcatgtct gggaactggg 180  
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<210> 33  
<211> 489  
<212> DNA  
<213> Homo sapiens

<400> 33

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<211> 276  
<212> DNA  
<213> Homo sapiens

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<210> 35  
<211> 516  
<212> DNA  
<213> Homo sapiens

<400> 35  
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gcattattgg cccatgcaaa aatgctggga ctgactgtaa gtttaattca agatgctgga 420  
cgtactcaga ttgcaccagg ctctcaaaact gtcctaggga ttgggcccagg accagcagac 480

516

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<210> 36  
<211> 447  
<212> DNA  
<213> Homo sapiens

<400> 36  
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ggtttccaaa acaaatgcta ttatttctct aaagaagaag gagattggaa ttcaagtaaa 180  
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aatggattt gcaggaaaag aatacac 447

<210> 37  
<211> 564  
<212> DNA  
<213> Homo sapiens

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gcagaagtgg aaaaacagag taaaaaattg gaaaagaaga aggaaacaat aacagagtca 180  
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<212> DNA

<213> Homo sapiens

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aaaaccaaga agctctacat tgacagtcgt gctcgaagaa atctaggctc catcaacact 420  
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cgccaggatg cgaagtactt gaacatgcgt tccacttatg ccaaacttgc agcagtagct 600  
gtatTTTTTca tcatgttaat agtgtatgtc cgattctggt ggctg 645

<210> 39  
<211> 336  
<212> DNA  
<213> Homo sapiens

<400> 39  
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gccaaagttg gagttagtat gttcaacaga ccccat 336

<210> 40  
<211> 342  
<212> DNA  
<213> Homo sapiens

<400> 40  
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gcagggtgc tcttcggcag tctagccggc ctgggtgctt accagctgta tcaggatcca 180



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<210> 41  
<211> 981  
<212> DNA  
<213> Homo sapiens

<400> 41  
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agaatgcgcg ggctcttttt c 981

<210> 42  
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<212> DNA  
<213> Homo sapiens

<400> 42  
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<210> 43  
<211> 549  
<212> DNA  
<213> Homo sapiens

<400> 43  
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gggcacattt acaaccagaa tgtatcccag aaggactgca actgcctgca cgtgggtggag 180  
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atgctcagc 549

<210> 44  
<211> 348  
<212> DNA  
<213> Homo sapiens

<400> 44  
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gccaaaatca atgaagctaa agatttacta gaaggtcaag ctaaaaaa 348

<210> 45  
<211> 456  
<212> DNA  
<213> Homo sapiens

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aaaagtggct tgggcagtgg acccaaatgc tgccat 456

<210> 46  
<211> 1677  
<212> DNA  
<213> Homo sapiens

<400> 46  
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<212> DNA

<213> Homo sapiens

<400> 47

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<210> 48

<211> 324

<212> DNA

<213> Homo sapiens

<400> 48

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ctgatcatca agaaaaaaga aact 324

<210> 49  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 49  
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ccc 303

<210> 50  
<211> 1116  
<212> DNA  
<213> Homo sapiens

<400> 50  
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<210> 51  
<211> 986  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
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<400> 51  
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Met Thr Gly Leu Ala Leu Leu Tyr Ser Gly  
1 5 10

gtc ttc gtg gcc ttc tgg gcc tgc gcg ctg gcc gtg gga gtc tgc tac 159  
Val Phe Val Ala Phe Trp Ala Cys Ala Leu Ala Val Gly Val Cys Tyr  
15 20 25

acc att ttt gat ttg ggc ttc cgc ttt gat gtg gca tgg ttc ctg acg 207  
Thr Ile Phe Asp Leu Gly Phe Arg Phe Asp Val Ala Trp Phe Leu Thr  
30 35 40

gag act tcg ccc ttc atg tgg tcc aac ctg ggc att ggc cta gct atc 255  
Glu Thr Ser Pro Phe Met Trp Ser Asn Leu Gly Ile Gly Leu Ala Ile  
45 50 55

tcc ctg tct gtg gtt ggg gca gcc tgg ggc atc tat att acc ggc tcc 303  
Ser Leu Ser Val Val Gly Ala Ala Trp Gly Ile Tyr Ile Thr Gly Ser  
60 65 70

tcc atc att ggt gga gga gtg aag gcc ccc agg atc aag acc aag aac 351  
Ser Ile Ile Gly Gly Val Lys Ala Pro Arg Ile Lys Thr Lys Asn  
75 80 85 90

ctg gtc agc atc atc ttc tgt gag gct gtg gcc atc tac ggc atc atc 399  
Leu Val Ser Ile Ile Phe Cys Glu Ala Val Ala Ile Tyr Gly Ile Ile  
95 100 105

atg gca att gtc att agc aac atg gct gag cct ttc agt gcc aca gac 447  
Met Ala Ile Val Ile Ser Asn Met Ala Glu Pro Phe Ser Ala Thr Asp  
110 115 120

ccc aag gcc atc ggc cat cgg aac tac cat gca ggc tac tcc atg ttt 495  
Pro Lys Ala Ile Gly His Arg Asn Tyr His Ala Gly Tyr Ser Met Phe  
125 130 135

ggg gct ggc ctc acc gta ggc ctg tct aac ctc ttc tgt gga gtc tgc 543  
Gly Ala Gly Leu Thr Val Gly Leu Ser Asn Leu Phe Cys Gly Val Cys

140 145 150

gtg ggc atc gtg ggc agt ggg gct gcc ctg gcc gat gct cag aac ccc 591  
Val Gly Ile Val Gly Ser Gly Ala Ala Leu Ala Asp Ala Gln Asn Pro  
155 160 165 170

agc ctc ttt gta aag att ctc atc gtg gag atc ttt ggc agc gcc att 639  
Ser Leu Phe Val Lys Ile Leu Ile Val Glu Ile Phe Gly Ser Ala Ile  
175 180 185

ggc ctc ttt ggg gtc atc gtc gca att ctt cag acc tcc aga gtg aag 687  
Gly Leu Phe Gly Val Ile Val Ala Ile Leu Gln Thr Ser Arg Val Lys  
190 195 200

atg ggt gac tagatgatat gtgtgggtgg ggccgtgcct cacttttatt 736  
Met Gly Asp  
205

tattgtctggt tttcctggga cagctggagc tgtgtccctt agcctttcag aggcttggtg 796

ttcaggggccc tccctgcact cccctcttgc tgcgtgttga tttggaggca ctgcagtcca 856

ggccgagtcc tcagtgcggg gagcaggctg ctgctgctga ctctgtgcag ctgcgcacct 916

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tgtctgggtc 986

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gccgcgcagc ggacaccgtg cgtaccggcc tgcggcgccc ggccaccggg gcggaccgcg 120

gaaccgcagg cc atg tcc cat gaa aag agt ttt ttg gtg tct ggg gac aac 171  
Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn  
1 5 10

tat cct ccc ccc aac cct gga tat ccg ggg ggg ccc cag cca ccc atg 219  
Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met  
15 20 25

ccc ccc tat gct cag cct ccc tac cct ggg gcc cct tac cca cag ccc 267  
Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro  
30 35 40 45

cct ttc cag ccc tcc ccc tac ggt cag cca ggg tac ccc cat ggc ccc 315  
Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro



50	55	60	
agc ccc tac ccc caa ggg ggc tac cca cag ggt ccc tac ccc caa ggg			363
Ser Pro Tyr Pro Gln Gly Gly Tyr	Pro Gln Gly Pro Tyr	Pro Gln Gly	
65	70	75	
ggc tac cca cag ggc ccc tac cca caa gag ggc tac cca cag ggc ccc			411
Gly Tyr Pro Gln Gly Pro Tyr	Pro Gln Glu Gly Tyr	Pro Gln Gly Pro	
80	85	90	
tac ccc caa ggg ggc tac ccc cag ggg cca tat ccc cag agc ccc ttc			459
Tyr Pro Gln Gly Gly Tyr	Pro Gln Gly Pro Tyr	Pro Gln Ser Pro Phe	
95	100	105	
ccc ccc aac ccc tat gga cag cca cag gtc ttc cca gga caa gac cct			507
Pro Pro Asn Pro Tyr	Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro		
110	115	120	125
gac tca ccc cag cat gga aac tac cag gag gag ggt ccc cca tcc tac			555
Asp Ser Pro Gln His Gly Asn Tyr	Gln Glu Glu Gly Pro Pro Ser Tyr		
130	135	140	
tat gac aac cag gac ttc cct gcc acc aac tgg gat gac aag agc atc			603
Tyr Asp Asn Gln Asp Phe Pro Ala	Thr Asn Trp Asp Asp Lys Ser Ile		
145	150	155	
cga cag gcc ttc atc cgc aag gtg ttc cta gtg ctg acc ttg cag ctg			651
Arg Gln Ala Phe Ile Arg Lys Val	Phe Leu Val Leu Thr Leu Gln Leu		
160	165	170	
tcg gtg acc ctg tcc acg gtg tct gtg ttc act ttt gtt gcg gag gtg			699
Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr	Phe Val Ala Glu Val		
175	180	185	
aag ggc ttt gtc cgg gag aat gtc tgg acc tac tat gtc tcc tat gct			747
Lys Gly Phe Val Arg Glu Asn Val Trp Thr	Tyr Tyr Val Ser Tyr Ala		
190	195	200	205
gtc ttc ttc atc tct ctc atc gtc ctc agc tgt tgt ggg gac ttc cgg			795
Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg			
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cga aag cac ccc tgg aac ctt gtt gca ctg tcg gtc ctg acc gcc agc			843
Arg Lys His Pro Trp Asn Leu Val	Ala Leu Ser Val Leu Thr Ala Ser		
225	230	235	
ctg tcg tac atg gtg ggg atg atc gcc agc ttc tac aac acc gag gca			891
Leu Ser Tyr Met Val Gly Met	Ile Ala Ser Phe Tyr Asn Thr Glu Ala		
240	245	250	
gtc atc atg gcc gtg ggc atc acc aca gcc gtc tgc ttc acc gtc gtc			939
Val Ile Met Ala Val Gly Ile Thr Thr Ala Val	Cys Phe Thr Val Val		
255	260	265	
atc ttc tcc atg cag acc cgc tac gac ttc acc tca tgc atg ggc gtg			987
Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe	Thr Ser Cys Met Gly Val		
270	275	280	285

ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc gcc att ctc tgc atc 1035  
Leu Leu Val Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile  
290 295 300

ttc atc cgg aac cgc atc ctg gag atc gtg tac gcc tca ctg ggc gct 1083  
Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala  
305 310 315

ctg ctc ttc acc tgc ttc ctc gca gtg gac acc cag ctg ctg ctg ggg 1131  
Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly  
320 325 330

aac aag cag ctg tcc ctg agc cca gaa gag tat gtg ttt gct gcg ctg 1179  
Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu  
335 340 345

aac ctg tac aca gac atc atc aac atc ttc ctg tac atc ctc acc atc 1227  
Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile  
350 355 360 365

att ggc cgc gcc aag gag tagccgagct ccagctcgct gtgcccgcctc 1275  
Ile Gly Arg Ala Lys Glu  
370

aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg tacttcccc 1335

ctctcttgct cccaggcaca gcctagggaa aaggatgcct ctctccaacc ctctgtatg 1395

tacactgcag atacttccat ttggaccgcg tgtggccaca gcatggcccc tttagtcctc 1455

ccgccccgc caagggggcac caaggccacg tttccgtgcc acctcctgtc tactcattgt 1515

tgcattgagc ctgtctgcca gccacccca gggactgggg gcagcaccag gtcccgggga 1575

gagggattga gccaagaggt gaggtgcac gtcttccctc ctgtcccagc tcccagcct 1635

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cggagtgggg gtcttatccc tgtgtgagc cctgagggca gagaggatgg catgtttcag 1755

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Met Leu Ser Leu Asp Phe Leu Asp Asp Val Arg Arg Met Asn Lys Arg 15  
1 5 10

cag ctc tat tat caa gtc cta aat ttt gga atg att gtc tca tcg gca 157  
Gln Leu Tyr Tyr Gln Val Leu Asn Phe Gly Met Ile Val Ser Ser Ala 30  
20 25

cta atg atc tgg aag ggg tta atg gta ata act gga agt gaa agt ccg 205  
Leu Met Ile Trp Lys Gly Leu Met Val Ile Thr Gly Ser Glu Ser Pro 45  
35 40

att gta gtg gtg ctc agt ggc agc atg gaa cct gca ttt cat aga gga 253  
Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala Phe His Arg Gly 60  
50 55

gat ctt ctc ttt cta aca aat cga gtt gaa gat ccc ata cga gtg gga 301  
Asp Leu Leu Phe Leu Thr Asn Arg Val Glu Asp Pro Ile Arg Val Gly 80  
65 70 75

gaa att gtt gtt ttt agg ata gaa gga aga gag att cct ata gtt cac 349  
Glu Ile Val Val Phe Arg Ile Glu Gly Arg Glu Ile Pro Ile Val His 95  
85 90

cga gtc ttg aag att cat gaa aag caa aat ggg cat atc aag ttt ttg 397  
Arg Val Leu Lys Ile His Glu Lys Gln Asn Gly His Ile Lys Phe Leu 110  
100 105

acc aaa gga gat aat aat gcg gtt gat gac cga ggc ctc tat aaa caa 445  
Thr Lys Gly Asp Asn Asn Ala Val Asp Asp Arg Gly Leu Tyr Lys Gln 125  
115 120

gga caa cat tgg cta gag aaa aaa gat gtt gtg ggg aga gcc agg gga 493  
Gly Gln His Trp Leu Glu Lys Lys Asp Val Val Gly Arg Ala Arg Gly 140  
130 135

ttt gtt cct tat att gga att gtg acg atc ctc atg aat gac tat cct 541  
Phe Val Pro Tyr Ile Gly Ile Val Thr Ile Leu Met Asn Asp Tyr Pro 160  
145 150

aaa ttt aag tat gca gtt ctc ttt ttg ctg ggt tta ttc gtg ctg gtt 589  
Lys Phe Lys Tyr Ala Val Leu Phe Leu Gly Leu Phe Val Leu Val 175  
165 170

cat cgt gag taagaagcct gccttgctgt tcctgggaag atgccatagt 638  
His Arg Glu

tttcgttact ggatgttttg agtagataact ggtctgtgat tgggtggaatg gagaacacac 698

gtgttggtgc ttctgggtag cactgggttg cattagttta tgtttccatg ccagagtttg 758

tgtgggcggg cgcattgtgca ccacagagt cactcgaggg gactttcagt cacaggattt 818

cataattgtc attgtcacac tttaaattt ttgtacatca gtgaattttt ttatattaaa 878

aggttgagcc aaagccccc gtgtttgtat ttggaagcca agcttcactt cttaaagtgcc 938

tacagagact tgtaaatgaa aatgcagctc tgcacgagtt tgaaaccgtc atacctcctt 998  
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aagactttgc acattgag 1076

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Met Ala Leu Leu Phe  
1 5

tcc ttg atc ctt gcc att tgc acc aga cct gga ttc cta gcg tct cca 164  
Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly Phe Leu Ala Ser Pro  
10 15 20

tct gga gtg cgg ctg gtg ggg ggc ctc cac cgc tgt gaa ggg cgg gtg 212  
Ser Gly Val Arg Leu Val Gly Gly Leu His Arg Cys Glu Gly Arg Val  
25 30 35

gag gtg gaa cag aaa ggc cag tgg ggc acc gtg tgt gat gac ggc tgg 260  
Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp  
40 45 50

gac att aag gac gtg gct gtg ttg tgc cgg gag ctg ggc tgt gga gct 308  
Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu Leu Gly Cys Gly Ala  
55 60 65

gcc agc gga acc cct agt ggt att ttg tat gag cca cca gca gaa aaa 356  
Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu Pro Pro Ala Glu Lys  
70 75 80 85

gag caa aag gtc ctc atc caa tca gtc agt tgc aca gga aca gaa gat 404  
Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys Thr Gly Thr Glu Asp  
90 95 100

aca ttg gct cag tgt gag caa gaa gaa gtt tat gat tgt tca cat gaa 452  
Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr Asp Cys Ser His Glu  
105 110 115

gaa gat gct ggg gca tgc tgt gag aac cca gag agc tct ttc tcc cca 500  
Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu Ser Ser Phe Ser Pro  
120 125 130

gtc cca gag ggt gtc agg ctg gct gac ggc cct ggg cat tgc aag gga 548

Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro Gly His Cys Lys Gly	135	140	145	
cgc gtg gaa gtg aag cac cag aac cag tgg tat acc gtg tgc cag aca	150	155	160	596
Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr Thr Val Cys Gln Thr				
ggc tgg agc ctc cgg gcc gca aag gtg gtg tgc cgg cag ctg gga tgt	170	175	180	644
Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys Arg Gln Leu Gly Cys				
ggg agg gct gta ctg act caa aaa cgc tgc aac aag cat gcc tat ggc	185	190	195	692
Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn Lys His Ala Tyr Gly				
cga aaa ccc atc tgg ctg agc cag atg tca tgc tca gga cga gaa gca	200	205	210	740
Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys Ser Gly Arg Glu Ala				
acc ctt cag gat tgc cct tct ggg cct tgg ggg aag aac acc tgc aac	215	220	225	788
Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly Lys Asn Thr Cys Asn				
cat gat gaa gac acg tgg gtc gaa tgt gaa gat ccc ttt gac ttg aga	230	235	240	836
His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp Pro Phe Asp Leu Arg				
cta gta gga gga gac aac ctc tgc tct ggg cga ctg gag gtg ctg cac	250	255	260	884
Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg Leu Glu Val Leu His				
aag ggc gta tgg ggc tct gtc tgt gat gac aac tgg gga gaa aag gag	265	270	275	932
Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn Trp Gly Glu Lys Glu				
gac cag gtg gta tgc aag caa ctg ggc tgt ggg aag tcc ctc tct ccc	280	285	290	980
Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly Lys Ser Leu Ser Pro				
tcc ttc aga gac cgg aaa tgc tat ggc cct ggg gtt ggc cgc atc tgg	295	300	305	1028
Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly Val Gly Arg Ile Trp				
ctg gat aat gtt cgt tgc tca ggg gag gag cag tcc ctg gag cag tgc	310	315	320	1076
Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln Ser Leu Glu Gln Cys				
cag cac aga ttt tgg ggg ttt cac gac tgc acc cac cag gaa gat gtg	330	335	340	1124
Gln His Arg Phe Trp Gly Phe His Asp Cys Thr His Gln Glu Asp Val				
gct gtc atc tgc tca gga tagtatactg gtgttgcttg acctggcccc	345			1172
Ala Val Ile Cys Ser Gly				
cctggccccg cctgccctct gcttggtctc ctgagccctg attatactca tactcattct				1232

ggggctcagg cttgagccac tactccctca tcccctcagg agtctgaaca ctgggcttat 1292  
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gtcagatgtg cagaccatta ctaaggtcta tgtctgcaaa cattactaat ctaggctcta 1532  
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Met Pro Thr Val Asp Asp Ile Leu  
1 5

gag cag gtt ggg gag tct ggc tgg ttc cag aag caa gcc ttc ctc atc 161  
Glu Gln Val Gly Glu Ser Gly Trp Phe Gln Lys Gln Ala Phe Leu Ile  
10 15 20

tta tgc ctg ctg tcg gct gcc ttt gcg ccc atc tgt gtg ggc atc gtc 209  
Leu Cys Leu Leu Ser Ala Ala Phe Ala Pro Ile Cys Val Gly Ile Val  
25 30 35 40

ttc ctg ggt ttc aca cct gac cac cac tgc cag agt cct ggg gtg gct 257  
Phe Leu Gly Phe Thr Pro Asp His His Cys Gln Ser Pro Gly Val Ala  
45 50 55

gag ctg agc cag cgc tgt ggc tgg agc cct gcg gag gag ctg aac tat 305  
Glu Leu Ser Gln Arg Cys Gly Trp Ser Pro Ala Glu Glu Leu Asn Tyr  
60 65 70

aca gtg cca ggc ctg ggg ccc gcg ggc gag gcc ttc ctt ggc cag tgc 353  
Thr Val Pro Gly Leu Gly Pro Ala Gly Glu Ala Phe Leu Gly Gln Cys  
75 80 85

agg cgc tat gaa gtg gac tgg aac cag agc gcc ctc agc tgt gta gac 401  
Arg Arg Tyr Glu Val Asp Trp Asn Gln Ser Ala Leu Ser Cys Val Asp  
90 95 100

ccc ctg gct agc ctg gcc acc aac agg agc cac ctg ccg ctg ggt ccc 449  
Pro Leu Ala Ser Leu Ala Thr Asn Arg Ser His Leu Pro Leu Gly Pro  
105 110 115 120

tgc cag gat ggc tgg gtg tat gac acg ccc ggc tct tcc atc gtc act 497  
Cys Gln Asp Gly Trp Val Tyr Asp Thr Pro Gly Ser Ser Ile Val Thr  
125 130 135

gag ttc aac ctg gtg tgt gct gac tcc tgg aag ctg gac ctc ttt cag 545  
Glu Phe Asn Leu Val Cys Ala Asp Ser Trp Lys Leu Asp Leu Phe Gln  
140 145 150

tcc tgt ttg aat gcg ggc ttc ttc ttt ggc tct ctc ggt gtt ggc tac 593  
Ser Cys Leu Asn Ala Gly Phe Phe Phe Gly Ser Leu Gly Val Gly Tyr  
155 160 165

ttt gca gac agg ttt ggc cgt aag ctg tgt ctc ctg gga act gtg ctg 641  
Phe Ala Asp Arg Phe Gly Arg Lys Leu Cys Leu Leu Gly Thr Val Leu  
170 175 180

gtc aac gcg gtg tcg ggc gtg ctc atg gcc ttc tcg ccc aac tac atg 689  
Val Asn Ala Val Ser Gly Val Leu Met Ala Phe Ser Pro Asn Tyr Met  
185 190 195 200

tcc atg ctg ctc ttc cgc ctg ctg cag ggc ctg gtc agc aag ggc aac 737  
Ser Met Leu Leu Phe Arg Leu Leu Gln Gly Leu Val Ser Lys Gly Asn  
205 210 215

tgg atg gct ggc tac acc cta atc aca gaa ttt gtt ggc tcg ggc tcc 785  
Trp Met Ala Gly Tyr Thr Leu Ile Thr Glu Phe Val Gly Ser Gly Ser  
220 225 230

aga aga acg gtg gcg atc atg tac cag atg gcc ttc acg gtg ggg ctg 833  
Arg Arg Thr Val Ala Ile Met Tyr Gln Met Ala Phe Thr Val Gly Leu  
235 240 245

gtg gcg ctt acc ggg ctg gcc tac gcc ctg cct cac tgg cgc tgg ctg 881  
Val Ala Leu Thr Gly Leu Ala Tyr Ala Leu Pro His Trp Arg Trp Leu  
250 255 260

cag ctg gca gtc tcc ctg ccc acc ttc ctc ttc ctg ctc tac tac tgg 929  
Gln Leu Ala Val Ser Leu Pro Thr Phe Leu Phe Leu Leu Tyr Tyr Trp  
265 270 275 280

tgt gtg ccg gag tcc cct cgg tgg ctg tta tca caa aaa aga aac act 977  
Cys Val Pro Glu Ser Pro Arg Trp Leu Leu Ser Gln Lys Arg Asn Thr  
285 290 295

gaa gca ata aag ata atg gac cac atc gct caa aag aat ggg aag ttg 1025  
Glu Ala Ile Lys Ile Met Asp His Ile Ala Gln Lys Asn Gly Lys Leu  
300 305 310

cct cct gct gat tta aag atg ctt tcc ctc gaa gag gat gtc acc gaa 1073  
Pro Pro Ala Asp Leu Lys Met Leu Ser Leu Glu Glu Asp Val Thr Glu  
315 320 325

aag ctg agc cct tca ttt gca gac ctg ttc cgc acg ccg cgc ctg agg 1121  
Lys Leu Ser Pro Ser Phe Ala Asp Leu Phe Arg Thr Pro Arg Leu Arg  
330 335 340

aag cgc acc ttc atc ctg atg tac ctg tgg ttc acg gac tct gtg ctc 1169

Lys Arg Thr Phe Ile Leu Met Tyr Leu Trp Phe Thr Asp Ser Val Leu  
345 350 355 360

tat cag ggg ctc atc ctg cac atg ggc gcc acc agc ggg aac ctc tac 1217  
Tyr Gln Gly Leu Ile Leu His Met Gly Ala Thr Ser Gly Asn Leu Tyr  
365 370 375

ctg gat ttc ctt tac tcc gct ctg gtc gaa atc ccg ggg gcc ttc ata 1265  
Leu Asp Phe Leu Tyr Ser Ala Leu Val Glu Ile Pro Gly Ala Phe Ile  
380 385 390

gcc ctc atc acc att gac cgc gtg ggc cgc atc tac ccc atg gcc gtg 1313  
Ala Leu Ile Thr Ile Asp Arg Val Gly Arg Ile Tyr Pro Met Ala Val  
395 400 405

tca aat ttg ttg gcg ggg gca gcc tgc ctc gtc atg att ttt atc tca 1361  
Ser Asn Leu Leu Ala Gly Ala Ala Cys Leu Val Met Ile Phe Ile Ser  
410 415 420

cct gac ctg cac tgg tta aac atc ata atc atg tgt gtt ggc cga atg 1409  
Pro Asp Leu His Trp Leu Asn Ile Ile Ile Met Cys Val Gly Arg Met  
425 430 435 440

gga atc acc att gca ata caa atg atc tgc ctg gtg aat gct gag ctg 1457  
Gly Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Ala Glu Leu  
445 450 455

tac ccc aca ttc gtc agg aac ctc gga gtg atg gtg tgt tcc tcc ctg 1505  
Tyr Pro Thr Phe Val Arg Asn Leu Gly Val Met Val Cys Ser Ser Leu  
460 465 470

tgt gac ata ggt ggg ata atc acc ccc ttc ata gtc ttc agg ctg agg 1553  
Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg  
475 480 485

gag gtc tgg caa gcc ttg ccc ctc att ttg ttt gcg gtg ttg ggc ctg 1601  
Glu Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu  
490 495 500

ctt gcc gcg gga gtg acg cta ctt ctt cca gag acc aag ggg gtc gct 1649  
Leu Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala  
505 510 515 520

ttg cca gag acc atg aag gac gcc gag aac ctt ggg aga aaa gca aag 1697  
Leu Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys  
525 530 535

ccc aaa gaa aac acg att tac ctt aag gtc caa acc tca gaa ccc tcg 1745  
Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser  
540 545 550

ggc acc tgagagagat gttttgcggc gatgtcgtgt tggagggatg aagatggagt 1801  
Gly Thr

tatcctctgc agaaattcct agacgccttc acttctctgt attcttcttc atacttcct 1861

acccccaaat taatatcagt cctaaag 1888



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cgtgtcgccc cgagtgctg cggccgccgc ggcacc atg gct gtg ttt gtc gtg 114
                                         Met Ala Val Phe Val Val
                                         1             5

ctc ctg gcg ttg gtg gcg ggt gtt ttg ggg aac gag ttt agt ata tta 162
Leu Leu Ala Leu Val Ala Gly Val Leu Gly Asn Glu Phe Ser Ile Leu
                        10             15             20

aaa tca cca ggg tct gtt gtt ttc cga aat gga aat tgg cct ata cca 210
Lys Ser Pro Gly Ser Val Val Phe Arg Asn Gly Asn Trp Pro Ile Pro
                        25             30             35

gga gag cgg atc cca gac gtg gct gca ttg tcc atg ggc ttc tct gtg 258
Gly Glu Arg Ile Pro Asp Val Ala Ala Leu Ser Met Gly Phe Ser Val
                        40             45             50

aaa gaa gac ctt tct tgg cca gga ctc gca gtg ggt aac ctg ttt cat 306
Lys Glu Asp Leu Ser Trp Pro Gly Leu Ala Val Gly Asn Leu Phe His
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cgt cct cgg gct acc gtc atg gtg atg gtg aag gga gtg aac aaa ctg 354
Arg Pro Arg Ala Thr Val Met Val Met Val Lys Gly Val Asn Lys Leu
                        75             80             85

gct cta ccc cca ggc agt gtc att tcg tac cct ttg gag aat gca gtt 402
Ala Leu Pro Pro Gly Ser Val Ile Ser Tyr Pro Leu Glu Asn Ala Val
                        90             95             100

cct ttt agt ctt gac agt gtt gca aat tcc att cac tcc tta ttt tct 450
Pro Phe Ser Leu Asp Ser Val Ala Asn Ser Ile His Ser Leu Phe Ser
                        105             110             115

gag gaa act cct gtt gtt ttg cag ttg gct ccc agt gag gaa aga gtg 498
Glu Glu Thr Pro Val Val Leu Gln Leu Ala Pro Ser Glu Glu Arg Val
                        120             125             130

tat atg gta ggg aag gca aac tca gtg ttt gaa gac ctt tca gtc acc 546
Tyr Met Val Gly Lys Ala Asn Ser Val Phe Glu Asp Leu Ser Val Thr
                        135             140             145             150

ttg cgc cag ctc cgt aat cgc ctg ttt caa gaa aac tct gtt ctc agt 594
Leu Arg Gln Leu Arg Asn Arg Leu Phe Gln Glu Asn Ser Val Leu Ser
                        155             160             165

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tca ctc ccc ctc aat tct ctg agt agg aac aat gaa gtt gac ctg ctc 642  
Ser Leu Pro Leu Asn Ser Leu Ser Arg Asn Asn Glu Val Asp Leu Leu  
170 175 180

ttt ctt tct gaa ctg caa gtg cta cat gat att tca agc ttg ctg tct 690  
Phe Leu Ser Glu Leu Gln Val Leu His Asp Ile Ser Ser Leu Leu Ser  
185 190 195

cgt cat aag cat cta gcc aag gat cat tct cct gat tta tat tca ctg 738  
Arg His Lys His Leu Ala Lys Asp His Ser Pro Asp Leu Tyr Ser Leu  
200 205 210

gag ctg gca ggt ttg gat gaa att ggg aag cgt tat ggg gaa gac tct 786  
Glu Leu Ala Gly Leu Asp Glu Ile Gly Lys Arg Tyr Gly Glu Asp Ser  
215 220 225 230

gaa caa ttc aga gat gct tct aag atc ctt gtt gac gct ctg caa aag 834  
Glu Gln Phe Arg Asp Ala Ser Lys Ile Leu Val Asp Ala Leu Gln Lys  
235 240 245

ttt gca gat gac atg tac agt ctt tat ggt ggg aat gca gtg gta gag 882  
Phe Ala Asp Asp Met Tyr Ser Leu Tyr Gly Gly Asn Ala Val Val Glu  
250 255 260

tta gtc act gtc aag tca ttt gac acc tcc ctc att agg aag aca agg 930  
Leu Val Thr Val Lys Ser Phe Asp Thr Ser Leu Ile Arg Lys Thr Arg  
265 270 275

act atc ctt gag gca aaa caa gcg aag aac cca gca agt ccc tat aac 978  
Thr Ile Leu Glu Ala Lys Gln Ala Lys Asn Pro Ala Ser Pro Tyr Asn  
280 285 290

ctt gca tat aag tat aat ttt gaa tat tcc gtg gtt ttc aac atg gta 1026  
Leu Ala Tyr Lys Tyr Asn Phe Glu Tyr Ser Val Val Phe Asn Met Val  
295 300 305 310

ctt tgg ata atg atc gcc ttg gcc ttg gct gtg att atc acc tct tac 1074  
Leu Trp Ile Met Ile Ala Leu Ala Leu Ala Val Ile Ile Thr Ser Tyr  
315 320 325

aat att tgg aac atg gat cct gga tat gat agc atc att tat agg atg 1122  
Asn Ile Trp Asn Met Asp Pro Gly Tyr Asp Ser Ile Ile Tyr Arg Met  
330 335 340

aca aac cag aag att cga atg gat tgaatgttac ctgtgccaga attagaaaag 1176  
Thr Asn Gln Lys Ile Arg Met Asp  
345 350

gggggttgaa attggctggt ttgttaaaat atatctttta gtgtgcttta aagtagatag 1236

tatactttac atttataaaa aaaaatcaaa ttttgttctt tattttgtgt gtgcctgtga 1296

tggttttcta gagtgaatta tagtattgac gtgaatccca ctgtggtata gattccataa 1356

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tgtgtaagtt actatggttt gtggtacaac ttcattctat agaattattaa gtggaagtgg 1956  
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cagcctttct ccaggttctg tctctcccat tctgattctt gacaccagat gcagg atg 178  
Met  
1

gtg tcc tct ccc tgc acg cag gca agc tca cgg act tgc tcc cgt atc 226  
Val Ser Ser Pro Cys Thr Gln Ala Ser Ser Arg Thr Cys Ser Arg Ile  
5 10 15

ctg gga ctg agc ctt ggg act gca gcc ctg ttt gct gct ggg gcc aac 274  
Leu Gly Leu Ser Leu Gly Thr Ala Ala Leu Phe Ala Ala Gly Ala Asn  
20 25 30

gtg gca ctc ctc ctt cct aac tgg gat gtc acc tac ctg ttg agg ggc 322  
Val Ala Leu Leu Leu Pro Asn Trp Asp Val Thr Tyr Leu Leu Arg Gly  
35 40 45

ctc ctt ggc agg cat gcc atg ctg gga act ggg ctc tgg gga gga ggc 370  
Leu Leu Gly Arg His Ala Met Leu Gly Thr Gly Leu Trp Gly Gly Gly  
50 55 60 65

ctc atg gta ctc act gca gct atc ctc atc tcc ttg atg ggc tgg aga 418  
Leu Met Val Leu Thr Ala Ala Ile Leu Ile Ser Leu Met Gly Trp Arg  
70 75 80

tac ggc tgc ttc agt aag agt ggg ctc tgt cga agc gtg ctt act gct 466  
Tyr Gly Cys Phe Ser Lys Ser Gly Leu Cys Arg Ser Val Leu Thr Ala  
85 90 95

ctg ttg tca ggt ggc ctg gct tta ctt gga gcc ctg att tgc ttt gtc 514  
Leu Leu Ser Gly Gly Leu Ala Leu Leu Gly Ala Leu Ile Cys Phe Val  
100 105 110

act tct gga gtt gct ctg aaa gat ggt cct ttt tgc atg ttt gat gtt 562  
Thr Ser Gly Val Ala Leu Lys Asp Gly Pro Phe Cys Met Phe Asp Val  
115 120 125

tca tcc ttc aat cag aca caa gct tgg aaa tat ggt tac cca ttc aaa 610  
Ser Ser Phe Asn Gln Thr Gln Ala Trp Lys Tyr Gly Tyr Pro Phe Lys  
130 135 140 145

gac ctg cat agt agg aat tat ctg tat gac cgt tgc ctc tgg aac tcc 658  
Asp Leu His Ser Arg Asn Tyr Leu Tyr Asp Arg Ser Leu Trp Asn Ser  
150 155 160

gtc tgc ctg gag ccc tct gca gct gtt gtc tgg cac gtg tcc ctc ttc 706  
Val Cys Leu Glu Pro Ser Ala Ala Val Val Trp His Val Ser Leu Phe  
165 170 175

tcc gcc ctt ctg tgc atc agc ctg ctc cag ctt ctc ctg gtg gtc gtt 754  
Ser Ala Leu Leu Cys Ile Ser Leu Leu Gln Leu Leu Leu Val Val Val  
180 185 190

cat gtc atc aac agc ctc ctg ggc ctt ttc tgc agc ctc tgc gag aag 802  
His Val Ile Asn Ser Leu Leu Gly Leu Phe Cys Ser Leu Cys Glu Lys  
195 200 205

tgacaggcag aaccttcact tgcaagcatg ggtgtttatc atcatcggct gtcttgaatc 862  
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1 5 10

gcg gca gcg gcg acg cga ggg ctc ccg gcc gcc cgc gtc cgc tgg gaa 99  
Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu

15	20	25	30	
tct agc ttc tcc agg act gtg gtc gcc ccg tcc gct gtg gcg gga aag				147
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys				
	35	40	45	
cgg ccc cca gaa ccg acc aca ccg tgg caa gag gac cca gaa ccc gag				195
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu				
	50	55	60	
gac gaa aac ttg tat gag aag aac cca gac tcc cat ggt tat gac aag				243
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys				
	65	70	75	
gac ccc gtt ttg gac gtc tgg aac atg cga ctt gtc ttc ttc ttt ggc				291
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly				
	80	85	90	
gtc tcc atc atc ctg gtc ctt ggc agc acc ttt gtg gcc tat ctg cct				339
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro				
	95	100	105	110
gac tac agg tgc aca ggg tgt cca aga gcg tgg gat ggg atg aaa gag				387
Asp Tyr Arg Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu				
	115	120	125	
tgg tcc cgc cgc gaa gct gag agg ctt gtg aaa tac cga gag gcc aat				435
Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn				
	130	135	140	
ggc ctt ccc atc atg gaa tcc aac tgc ttc gac ccc agc aag atc cag				483
Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln				
	145	150	155	
ctg cca gag gat gag tgaccagttg ctaagtgggg ctcaagaagc accgccttcc				538
Leu Pro Glu Asp Glu				
	160			
ccaccccctg cctgccattc tgacctcttc tcagagcacc taattaaagg ggctgaaagt				598
				601
ctg				
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Leu Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val 15  
5 10

gcc ctg acc acg gga gcc ttg ggc ctg gag ctg ccc ttg tcc tgc cag 151  
Ala Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln 35  
20 25 30

gaa gtc ctg tgg cca ctg ccc gcc tac ttg ctg gtg tcc gcc ggc tgc 199  
Glu Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys 50  
40 45

tat gcc ctg ggc act gtg ggc tat cgt gtg gcc act ttt cat gac tgc 247  
Tyr Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys 65  
55 60

gag gac gcc gca cgc gag ctg cag agc cag ata cag gag gcc cga gcc 295  
Glu Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala 80  
70 75

gac tta gcc cgc agg ggg ctg cgc ttc tgacagccta accccattcc 342  
Asp Leu Ala Arg Arg Gly Leu Arg Phe 90  
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tgtgaggaca gcccttcctc ccatttccca ttaaagagcc agtttatattt ct 394

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Met Glu Tyr Leu Ala His Pro Ser Thr Leu 10  
1 5

ggc ttg gct gtt gga gtt gct tgt ggc atg tgc ctg ggc tgg agc ctt 159  
Gly Leu Ala Val Gly Val Ala Cys Gly Met Cys Leu Gly Trp Ser Leu 25  
15 20

cga gta tgc ttt ggg atg ctc ccc aaa agc aag acg agc aag aca cac 207  
Arg Val Cys Phe Gly Met Leu Pro Lys Ser Lys Thr Ser Lys Thr His 40  
30 35

aca gat act gaa agt gaa gca agc atc ttg gga gac agc ggg gag tac 255  
Thr Asp Thr Glu Ser Glu Ala Ser Ile Leu Gly Asp Ser Gly Glu Tyr 55  
45 50

aag atg att ctt gtg gtt cga aat gac tta aag atg gga aaa ggg aaa 303  
Lys Met Ile Leu Val Val Arg Asn Asp Leu Lys Met Gly Lys Gly Lys

60	65	70	
gtg gct gcc cag tgc tct cat gct gct gtt tca gcc tac aag cag att			351
Val Ala Ala Gln Cys Ser His Ala Ala Val Ser Ala Tyr Lys Gln Ile			90
75	80	85	
caa aga aga aat cct gaa atg ctc aaa caa tgg gaa tac tgt ggc cag			399
Gln Arg Arg Asn Pro Glu Met Leu Lys Gln Trp Glu Tyr Cys Gly Gln			105
	95	100	
ccc aag gtg gtg gtc aaa gct cct gat gaa gaa acc ctg att gca tta			447
Pro Lys Val Val Val Lys Ala Pro Asp Glu Glu Thr Leu Ile Ala Leu			120
	110	115	
ttg gcc cat gca aaa atg ctg gga ctg act gta agt tta att caa gat			495
Leu Ala His Ala Lys Met Leu Gly Leu Thr Val Ser Leu Ile Gln Asp			135
	125	130	
gct gga cgt act cag att gca cca ggc tct caa act gtc cta ggg att			543
Ala Gly Arg Thr Gln Ile Ala Pro Gly Ser Gln Thr Val Leu Gly Ile			150
	140	145	
ggg cca gga cca gca gac cta att gac aaa gtc act ggt cac cta aaa			591
Gly Pro Gly Pro Ala Asp Leu Ile Asp Lys Val Thr Gly His Leu Lys			170
	155	160	
ctt tac taggtggact ttgatatgac aacaaccct ccatcacaag tgtttgaagc			647
Leu Tyr			
ctgtcagatt ctaacaacaa aagctgaatt tcttcacca acttaaagt tcttgagatg			707
			732
aaaataaaaac ctattcccat gttct			
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aataaagtta caactttgaa gagagtttct gcaagacatg acacaaagct gctagcagaa			120
aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt			174
	Met Met Thr Lys His Lys Lys Cys		
	1	5	
ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata			222
Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile			20
	10	15	
ggt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att			270

Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile  
25 30 35 40

ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318  
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp  
45 50 55

aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata 366  
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile  
60 65 70

att gac aac ata gaa gaa atg aat ttt ctt agg cgg tat aaa tgc agt 414  
Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser  
75 80 85

tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa 462  
Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln  
90 95 100

tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt 510  
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser  
105 110 115 120

gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt 558  
Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys  
125 130 135

tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taagttaatg 607  
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His  
140 145

tctaagataa tggggaaaat agaaaataac attattaagt gtaaaaccag caaagtactt 667  
697

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cagagacgaa ggtgcgag atg agc act atg ttc gcg gac act ctc ctc atc 171  
Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile  
1 5 10

gtt ttt atc tct gtg tgc acg gct ctg ctc gca gag ggc ata acc tgg 219  
Val Phe Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp  
15 20 25



gtc ctg gtt tac agg aca gac aag tac aag aga ctg aag gca gaa gtg 267  
Val Leu Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val  
30 35 40

gaa aaa cag agt aaa aaa ttg gaa aag aag aag gaa aca ata aca gag 315  
Glu Lys Gln Ser Lys Lys Leu Glu Lys Lys Lys Glu Thr Ile Thr Glu  
45 50 55

tca gct ggt cga caa cag aaa aag aaa ata gag aga caa gaa gag aaa 363  
Ser Ala Gly Arg Gln Gln Lys Lys Lys Ile Glu Arg Gln Glu Glu Lys  
60 65 70 75

ctg aag aat aac aac aga gat cta tca atg gtt cga atg aaa tcc atg 411  
Leu Lys Asn Asn Asn Arg Asp Leu Ser Met Val Arg Met Lys Ser Met  
80 85 90

ttt gct att ggc ttt tgt ttt act gcc cta atg gga atg ttc aat tcc 459  
Phe Ala Ile Gly Phe Cys Phe Thr Ala Leu Met Gly Met Phe Asn Ser  
95 100 105

ata ttt gat ggt aga gtg gtg gca aag ctt cct ttt acc cct ctt tct 507  
Ile Phe Asp Gly Arg Val Val Ala Lys Leu Pro Phe Thr Pro Leu Ser  
110 115 120

tac atc caa gga ctg tct cat cga aat ctg ctg gga gat gac acc aca 555  
Tyr Ile Gln Gly Leu Ser His Arg Asn Leu Leu Gly Asp Asp Thr Thr  
125 130 135

gac tgt tcc ttc att ttc ctg tat att ctc tgt act atg tcg att cga 603  
Asp Cys Ser Phe Ile Phe Leu Tyr Ile Leu Cys Thr Met Ser Ile Arg  
140 145 150 155

cag aac att cag aag att ctc ggc ctt gcc cct tca cga gcc gcc acc 651  
Gln Asn Ile Gln Lys Ile Leu Gly Leu Ala Pro Ser Arg Ala Ala Thr  
160 165 170

aag cag gca ggt gga ttt ctt ggc cca cca cct cct tct ggg aag ttc 699  
Lys Gln Ala Gly Gly Phe Leu Gly Pro Pro Pro Pro Ser Gly Lys Phe  
175 180 185

tct tgaactcaag aactctttat tttctatcat tctttctaga cacacacaca 752  
Ser

tcagactggc aactgttttg tagcaagagc cataggtagc cttactactt gggcctcttt 812

ctagttttga attatttcta agccttttgg gtatgattag agtgaaaatg gcagccagca 872

aacttgatag tgcttttggt cctagatgat ttttatcaaa taagtggatt gattagttaa 932

gttcaggtaa tgtttatgta atgaaaaaca aatagcatcc ttcttgtttc atttacataa 992

gtattttctg tgggaccgac totcaaggca ctgtgtatgc cctgcaagtt ggctgtctat 1052

gagcatttag agatttagaa gaaaaattta gtttgtttaa cccttgtaac tgtttgtttt 1112

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1186

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Met Val Leu Leu Thr Met Ile Ala Arg Val  
1 5 10

gcg gac ggg ctc ccg ctg gcc gcc tcg atg cag gag gac gaa cag tct 159  
Ala Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser  
15 20 25

ggc cgg gac ctt caa cag tat cag agt cag gct aag caa ctc ttt cga 207  
Gly Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg  
30 35 40

aag ttg aat gaa cag tcc cct acc aga tgt acc ttg gaa gca gga gcc 255  
Lys Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala  
45 50 55

atg act ttt cac tac att att gag cag ggg gtg tgt tat ttg gtt tta 303  
Met Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu  
60 65 70

tgt gaa gct gcc ttc cct aag aag ttg gct ttt gcc tac cta gaa gat 351  
Cys Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp  
75 80 85 90

ttg cac tca gaa ttt gat gaa cag cat gga aag aag gtg ccc act gtg 399  
Leu His Ser Glu Phe Asp Glu Gln His Gly Lys Lys Val Pro Thr Val  
95 100 105

tcc cga ccc tat tcc ttt att gaa ttt gat act ttc att cag aaa acc 447  
Ser Arg Pro Tyr Ser Phe Ile Glu Phe Asp Thr Phe Ile Gln Lys Thr  
110 115 120

aag aag ctc tac att gac agt cgt gct cga aga aat cta ggc tcc atc 495  
Lys Lys Leu Tyr Ile Asp Ser Arg Ala Arg Arg Asn Leu Gly Ser Ile  
125 130 135

aac act gaa ttg caa gat gtg cag agg atc atg gtg gcc aat att gaa 543  
Asn Thr Glu Leu Gln Asp Val Gln Arg Ile Met Val Ala Asn Ile Glu  
140 145 150

gaa gtg tta caa cga gga gaa gca ctc tca gca ttg gat tca aag gct 591

Glu Val Leu Gln Arg Gly Glu Ala Leu Ser Ala Leu Asp Ser Lys Ala  
155 160 165 170  
aac aat ttg tcc agt ctg tcc aag aaa tac cgc cag gat gcg aag tac 639  
Asn Asn Leu Ser Ser Leu Ser Lys Lys Tyr Arg Gln Asp Ala Lys Tyr  
175 180 185  
ttg aac atg cgt tcc act tat gcc aaa ctt gca gca gta gct gta ttt 687  
Leu Asn Met Arg Ser Thr Tyr Ala Lys Leu Ala Ala Val Ala Val Phe  
190 195 200  
ttc atc atg tta ata gtg tat gtc cga ttc tgg tgg ctg tgaaataatg 736  
Phe Ile Met Leu Ile Val Tyr Val Arg Phe Trp Trp Leu  
205 210 215  
aatacagtca ctggtaaggg agaacctaga acccagtagg tgtatatattt caggaaactg 796  
agctcacaga gatgtgtatt agaatccaag tggaacttct gcctctaaag accttgcaag 856  
aaaagagatg ccctgaaaat gaaaggttgc acctcattta atgaagctta accctatgta 916  
gaaagtctct ttcgggggca gaggctttct ctgggtgccca agccatatat attagggat 976  
agtagattgt taatttcgtt ttttccctcc cagtgcattt taaaaacagc actggctggg 1036  
gcattctcat tctctgatgg agccatcaat gagatttaac ttagtcaacc tgtgctagca 1096  
acattctgaa attccttcaa agaaggcagt cctttgggaa ggtgtttttt tttttttttt 1156  
tttttttgac tctaatacaac attccttttg ttggtgacat ttgtgatttt cagtaatctg 1216  
agtttttgat ggcccttttaa acaagactcc agtatgtgaa ggtaattgc tgtgctccac 1276  
agatcttgtc tattggcccc ttagaaaagt taacctttgt tgttttcctt ttataatttg 1336  
cttattgcac aattgcttta gggtaagtga attatattaa gatgcctga aattatagca 1396  
ctccttgatt aag 1409

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<212> DNA  
<213> Homo sapiens

<220>  
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cggcgacacc tcgcagtcac tcttgcggtc tgcgcgcct ttagacagc cggggccttc 120  
gtgagaccgg tgcaggcctg gggtagctc ctgtctggac agagaagaga aaa atg 176  
Met  
1

cag gac act ggc tca gta gtg cct ttg cat tgg ttt ggc ttt ggc tac 224  
Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly Tyr  
5 10 15

gca gca ctg gtt gct tct ggt ggg atc att ggc tat gta aaa gca ggc 272  
Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala Gly  
20 25 30

agc gtg ccg tcc ctg gct gca ggg ctg ctc ttt ggc agt cta gcc ggc 320  
Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala Gly  
35 40 45

ctg ggt gct tac cag ctg tct cag gat cca agg aac gtt tgg gtt ttc 368  
Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val Phe  
50 55 60 65

cta gct aca tct ggt acc ttg gct ggc att atg gga atg agg ttc tac 416  
Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe Tyr  
70 75 80

cac tct gga aaa ttc atg cct gca ggt tta att gca ggt gcc agt ttg 464  
His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser Leu  
85 90 95

ctg atg gtc gcc aaa gtt gga gtt agt atg ttc aac aga ccc cat 509  
Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His  
100 105 110

tagcagaagt catgttccag cttagactga tgaagaatta aaaatctgca tcttccacta 569  
ttttcaatat attaagagaa ataagtgcag catttttgca tctgacattt tacctaataa 629  
aaaagacacc aaacttgga gagaggtgga aaatcagtca tgattacaaa cctacagagg 689  
tggcgagtat gtaacacaag agcttaataa gaccctcata gagcttgatt cttgtatatt 749  
gatgttgtct tttctttctg tatctgtagg taaatctcaa gggtaaaatg ttaggtgtca 809  
gctttcaggg ctctgaaacc ctattccctg ctctgaggaa cagtgtgaaa aaaagtcttt 869  
taggagattt acaatatctg ttcttttgct catcttagac cacagactga ctttgaaatt 929  
atgttaagtg aaatatcaat gtaaataaag ttactataa ataata 974

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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (121)..(462)

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ccgcgggcct tcggcagatg caggcctggg gtagtctcct ttctggactg agaagagaag 120
atg gag aag ccc ctc ttc cca tta gtg cct ttg cat tgg ttt ggc ttt 168
Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly Phe
1 5 10 15
ggc tac aca gca ctg gtt gtt tct ggt ggg atc gtt ggc tat gta aaa 216
Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val Lys
20 25 30
aca ggc agc gtg ccg tcc ctg gca gca ggg ctg ctc ttc ggc agt cta 264
Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu
35 40 45
gcc ggc ctg ggt gct tac cag ctg tat cag gat cct agg aac gtt tgg 312
Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val Trp
50 55 60
ggt ttc cta gcc gct aca tct gtt act ttt gtt ggt gtt atg gga ata 360
Gly Phe Leu Ala Ala Thr Ser Val Thr Phe Val Gly Val Met Gly Ile
65 70 75 80
aga tcc tac tac tat gga aaa ttc atg cct gta ggt tta att gca ggt 408
Arg Ser Tyr Tyr Tyr Gly Lys Phe Met Pro Val Gly Leu Ile Ala Gly
85 90 95
gcc agt ttg ctg atg gcc gcc aaa gtt gga gtt cgt atg ttg atg aca 456
Ala Ser Leu Leu Met Ala Ala Lys Val Gly Val Arg Met Leu Met Thr
100 110
tct gat tagcagaagt catgttcgca gcttggactc atgaaggatt aaaaatctgc 512
Ser Asp
atcttccact attttcaatg tattaagaga aataagtgca gcatttttgc atctgacatt 572
ttacctaaaa aaaaaaagac accaaatttg gcggagggggt ggaaaatcag ttgttaccat 632
tataacccta cagaggtggt gagcatgtaa catgagctta ttgagaccat catagagatc 692
gattcttgta tattgatttt atctctttct gtatctatag gttaaattca agggtaaaat 752
gttaggtggt gacattgaga accctgaaac ccattccct gctcagagga acagtgtgaa 812
aaaaaatctc ttgagagatt tagaatatct tttcttttgc tcatcttaga ccacagactg 872
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<212> DNA  
<213> Homo sapiens

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Met Ala Ala Ala Ala Ala Ala Ala Thr Asn Gly Thr  
1 5 10

gga gga agc agc ggg atg gag gtg gat gca gca gta gtc ccc agc gtg 99  
Gly Gly Ser Ser Gly Met Glu Val Asp Ala Ala Val Val Pro Ser Val  
15 20 25 30

atg gcc tgc gga gtg act ggg agt gtt tcc gtc gct ctc cat ccc ctt 147  
Met Ala Cys Gly Val Thr Gly Ser Val Ser Val Ala Leu His Pro Leu  
35 40 45

gtc att ctc aac atc tca gac cac tgg atc cgc atg cgc tcc cag gag 195  
Val Ile Leu Asn Ile Ser Asp His Trp Ile Arg Met Arg Ser Gln Glu  
50 55 60

ggg cgg cct gtg cag gtg att ggg gct ctg att ggc aag cag gag ggc 243  
Gly Arg Pro Val Gln Val Ile Gly Ala Leu Ile Gly Lys Gln Glu Gly  
65 70 75

cga aat atc gag gtg atg aac tcc ttt gag ctg ctg tcc cac acc gtg 291  
Arg Asn Ile Glu Val Met Asn Ser Phe Glu Leu Leu Ser His Thr Val  
80 85 90

gaa gag aag att atc att gac aag gaa tat tat tac acc aag gag gag 339  
Glu Glu Lys Ile Ile Ile Asp Lys Glu Tyr Tyr Tyr Thr Lys Glu Glu  
95 100 105 110

cag ttt aaa cag gtg ttc aag gag ctg gag ttt ctg ggt tgg tat acc 387  
Gln Phe Lys Gln Val Phe Lys Glu Leu Glu Phe Leu Gly Trp Tyr Thr  
115 120 125

aca ggg ggg cca cct gac ccc tcg gac atc cac gtc cat aag cag gtg 435  
Thr Gly Gly Pro Pro Asp Pro Ser Asp Ile His Val His Lys Gln Val  
130 135 140

tgt gag atc atc gag agc ccc ctc ttt ctg aag ttg aac cct atg acc 483  
Cys Glu Ile Ile Glu Ser Pro Leu Phe Leu Lys Leu Asn Pro Met Thr  
145 150 155

aag cac aca gat ctt cct gtc agc gtt ttt gag tct gtc att gat ata 531  
Lys His Thr Asp Leu Pro Val Ser Val Phe Glu Ser Val Ile Asp Ile  
160 165 170

atc aat gga gag gcc aca atg ctg ttt gct gag ctg acc tac act ctg 579  
Ile Asn Gly Glu Ala Thr Met Leu Phe Ala Glu Leu Thr Tyr Thr Leu  
175 180 185 190

gcc aca gag gaa gcg gaa cgc att ggt gta gac cac gta gcc cga atg 627  
Ala Thr Glu Glu Ala Glu Arg Ile Gly Val Asp His Val Ala Arg Met  
195 200 205

aca gca aca ggc agt gga gag aac tcc act gtg gct gaa cac ctg ata 675  
Thr Ala Thr Gly Ser Gly Glu Asn Ser Thr Val Ala Glu His Leu Ile  
210 215 220

gca cag cac agc gcc atc aag atg ctg cac agc cgc gtc aag ctc atc 723  
Ala Gln His Ser Ala Ile Lys Met Leu His Ser Arg Val Lys Leu Ile  
225 230 235

ttg gag tac gtc aag gcc tct gaa gcg gga gag gtc ccc ttt aat cat 771  
Leu Glu Tyr Val Lys Ala Ser Glu Ala Gly Glu Val Pro Phe Asn His  
240 245 250

gag atc ctg cgg gag gcc tat gct ctg tgt cac tgt ctc ccg gtg ctc 819  
Glu Ile Leu Arg Glu Ala Tyr Ala Leu Cys His Cys Leu Pro Val Leu  
255 260 265 270

agc aca gac aag ttc aag aca gat ttt tat gat caa tgc aac gac gtg 867  
Ser Thr Asp Lys Phe Lys Thr Asp Phe Tyr Asp Gln Cys Asn Asp Val  
275 280 285

ggg ctc atg gcc tac ctc ggc acc atc acc aaa acg tgc aac acc atg 915  
Gly Leu Met Ala Tyr Leu Gly Thr Ile Thr Lys Thr Cys Asn Thr Met  
290 295 300

aac cag ttt gtg aac aag ttc aat gtc ctc tac gac cga caa ggc atc 963  
Asn Gln Phe Val Asn Lys Phe Asn Val Leu Tyr Asp Arg Gln Gly Ile  
305 310 315

ggc agg aga atg cgc ggg ctc ttt ttc tgatgagggg acttgaaggg 1010  
Gly Arg Arg Met Arg Gly Leu Phe Phe  
320 325

ctgatggaca ggggtcaggc aactatccca aaggggaggg cactacactt ccttgagaga 1070  
aaccactgtc attaataaaa ggggagcagc ccctgagcac ccctg 1115

<210> 67  
<211> 1721  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (6)..(1124)

<400> 67  
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Met Thr Leu Cys Ala Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu  
1 5 10 15

aac tcc ttc ctg cat cag agg atc ccc cag tcc gta cgg atc ctg ggc 98  
Asn Ser Phe Leu His Gln Arg Ile Pro Gln Ser Val Arg Ile Leu Gly.  
20 25 30

agc ctg gtg gcc atc ctg ctg gtg ttt ctg atc act gcc atc ctg gtg 146  
Ser Leu Val Ala Ile Leu Leu Val Phe Leu Ile Thr Ala Ile Leu Val  
35 40 45

aag gtg cag ctg gat gct ctg ccc ttc ttt gtc atc acc atg atc aag 194

Lys Val Gln Leu Asp Ala Leu Pro Phe Phe Val Ile Thr Met Ile Lys  
50 55 60

atc gtg ctc att aat tca ttt ggt gcc atc ctg cag ggc agc ctg ttt 242  
Ile Val Leu Ile Asn Ser Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe  
65 70 75

ggg ctg gct ggc ctt ctg cct gcc agc tac acg gcc ccc atc atg agt 290  
Gly Leu Ala Gly Leu Leu Pro Ala Ser Tyr Thr Ala Pro Ile Met Ser  
80 85 90 95

ggc cag ggc cta gca ggc ttc ttt gcc tcc gtg gcc atg atc tgc gct 338  
Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile Cys Ala  
100 105 110

att gcc agt ggc tgc gag cta tca gaa agt gcc ttc ggc tac ttt atc 386  
Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr Phe Ile  
115 120 125

aca gcc tgt gct gtt atc att ttg acc atc atc tgt tac ctg ggc ctg 434  
Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu Gly Leu  
130 135 140

ccc cgc ctg gaa ttc tac cgc tac tac cag cag ctc aag ctt gaa gga 482  
Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu Glu Gly  
145 150 155

ccc ggg gag cag gag acc aag ttg gac ctc att agc aaa gga gag gag 530  
Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly Glu Glu  
160 165 170 175

cca aga gca ggc aaa gag gaa tct gga gtt tca gtc tcc aac tct cag 578  
Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn Ser Gln  
180 185 190

ccc acc aat gaa agc cac tct atc aaa gcc atc ctg aaa aat atc tca 626  
Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn Ile Ser  
195 200 205

gtc ctg gct ttc tct gtc tgc ttc atc ttc act atc acc att ggg atg 674  
Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile Gly Met  
210 215 220

ttt cca gcc gtg act gtt gag gtc aag tcc agc atc gca ggc agc agc 722  
Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly Ser Ser  
225 230 235

acc tgg gaa cgt tac ttc att cct gtg tcc tgt ttc ttg act ttc aat 770  
Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr Phe Asn  
240 245 250 255

atc ttt gac tgg ttg ggc cgg agc ctc aca gct gta ttc atg tgg cct 818  
Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met Trp Pro  
260 265 270

ggg aag gac agc cgc tgg ctg cca agc ctg gtg ctg gcc cgg ctg gtg 866  
Gly Lys Asp Ser Arg Trp Leu Pro Ser Leu Val Leu Ala Arg Leu Val



275 280 285  
ttt gtg cca ctg ctg ctg ctg tgc aac att aag ccc cgc cgc tac ctg 914  
Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg Tyr Leu  
290 295 300  
act gtg gtc ttc gag cac gat gcc tgg ttc atc ttc ttc atg gct gcc 962  
Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met Ala Ala  
305 310 315  
ttt gcc ttc tcc aac ggc tac ctc gcc agc ctc tgc atg tgc ttc ggg 1010  
Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys Phe Gly  
320 325 330 335  
ccc aag aaa gtg aag cca gct gag gca gag acc gca gga gcc atc atg 1058  
Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Gly Ala Ile Met  
340 345 350  
gcc ttc ttc ctg tgt ctg ggt ctg gca ctg ggg gct gtt ttc tcc ttc 1106  
Ala Phe Phe Leu Cys Leu Gly Leu Ala Leu Gly Ala Val Phe Ser Phe  
355 360 365  
ctg ttc cgg gca att gtg tgacaaagga tggacagaag gactgcctgc 1154  
Leu Phe Arg Ala Ile Val  
370  
ctccctccct gtctgcctcc tgcccttcc ttctgccagg ggtgatcctg agtggctctgg 1214  
cggttttttc ttctaactga cttctgcttt ccacggcgtg tgctgggccc ggcctccag 1274  
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gagctggggtc tgaccgttgt atggtttgac ctgatatact ccattctccc ctgcgcctcc 1574  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (63)..(611)

<400> 68

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Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val 15  
1 5 10  
ccc cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc 155  
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys 30  
20 25  
atc tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat 203  
Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn 45  
35 40  
gta tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca 251  
Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro 60  
50 55  
gtg cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg 299  
Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg 75  
65 70  
tac gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac 347  
Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr 95  
80 85 90  
ctg tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg 395  
Leu Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu 110  
100 105  
gtg gac cct ctg atc cga aag ccg gat gca tac act gag caa ctg cac 443  
Val Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His 125  
115  
aat gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca 491  
Asn Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala 140  
130 135  
tcc ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt 539  
Ser Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly 155  
145 150  
gcc cag cag cgg tgg aag ctgcag gtg cag gag cag cgg aag aca gtc 587  
Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val 175  
160 165 170  
ttc gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 641  
Phe Asp Arg His Lys Met Leu Ser 180  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc 701  
tcggttccag tcttcccttt aaaagcctgt ggcatTTTTc ctcccttctcc ctaactttag 761  
aaatgttgta cttggctatt ttgattaggg aagagggatg tggctctctga tctctgttgt 821  
cttcttgggt ctttgggggt gaagggaggg ggaaggcagg ccagaaggga atggagacat 881

tcgaggcggc ctcaggagtg gatgcgatct gtctctcttg gctccactct tgccgccttc 941  
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cagtgtctgg gaggaagca tggcccagca ttcagcatgt gttcctttct gcagtgggtc 1061  
ttatcaccac ctccctccca gcccagcgc ctcagcccca gcccagctc cagccctgag 1121  
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tgtccacagt cactgagcca gacggtcggg ttgaacatga gactcgaggc tgagcgtgga 1361  
tctgaacacc acagcccctg tacttgggtt gcctcttgct cctgaacttc gttgtaccag 1421  
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cattaaattg ttttatttct ctc 1504

<210> 69  
<211> 532  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (93)..(440)

<400> 69  
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cccgttgga gcaagggagc ccagccggag cc atg gcc agt aca gtg gta gca 113  
Met Ala Ser Thr Val Val Ala  
1 5

gtt gga ctg acc att gct gct gca gga ttt gca ggc cgt tac gtt ttg 161  
Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly Arg Tyr Val Leu  
10 15 20

caa gcc atg aag cat atg gag cct caa gta aaa caa gtt ttt caa agc 209  
Gln Ala Met Lys His Met Glu Pro Gln Val Lys Gln Val Phe Gln Ser  
25 30 35

cta cca aaa tct gcc ttc agt ggt ggc tat tat aga ggt ggg ttt gaa 257  
Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg Gly Gly Phe Glu  
40 45 50 55

ccc aaa atg aca aaa cgg gaa gca gca tta ata cta ggt gta agc cct 305  
Pro Lys Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Ser Pro  
60 65 70

act gcc aat aaa ggg aaa ata aga gat gct cat cga cga att atg ctt 353

Thr Ala Asn Lys Gly Lys Ile Arg Asp Ala His Arg Arg Ile Met Leu  
75 80 85  
tta aat cat cct gac aaa gga gga tct cct tat ata gca gcc aaa atc 401  
Leu Asn His Pro Asp Lys Gly Gly Ser Pro Tyr Ile Ala Ala Lys Ile  
90 95 100  
aat gaa gct aaa gat tta cta gaa ggt caa gct aaa aaa tgaagtaaat 450  
Asn Glu Ala Lys Asp Leu Leu Glu Gly Gln Ala Lys Lys  
105 110 115  
gtatgatgaa ttttaagttc gtattagttt atgtatatga gtactaagtt tttataataa 510  
532  
aatgcctcag agctacaatt tt

<210> 70  
<211> 662  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (92)..(547)

<400> 70  
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tccagctggt cgaaggtgat ccagacgcaa g atg gct gtc ctc tct aag gaa 112  
Met Ala Val Leu Ser Lys Glu  
1 5

tat ggt ttt gtg ctt cta act ggt gct gcc agc ttt ata atg gtg gcc 160  
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala  
10 15 20

cac cta gcc atc aat gtt tcc aag gcc cgc aag aag tac aaa gtg gag 208  
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu  
25 30 35

tat cct atc atg tac agc acg gac cct gaa aat ggg cac atc ttc aac 256  
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn  
40 45 50 55

tgc att cag cga gcc cac cag aac acg ttg gaa gtg tat cct ccc ttc 304  
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Pro Phe  
60 65 70

tta ttt ttt cta gct gtt gga ggt gtt tac cac ccg cgt ata gct tct 352  
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser  
75 80 85

ggc ctg ggc ttg gcc tgg att gtt gga cga gtt ctt tat gct tat ggc 400  
Gly Leu Gly Leu Ala Trp Ile Val Gly Arg Val Leu Tyr Ala Tyr Gly  
90 95 100

tat tac acg gga gaa ccc agc aag cgt agt cga gga gcc ctg ggg tcc 448

Tyr Tyr Thr Gly Glu Pro Ser Lys Arg Ser Arg Gly Ala Leu Gly Ser  
105 110 115

atc gcc ctc ctg ggc ttg gtg ggc aca act gtg tgc tct gct ttc cag 496  
Ile Ala Leu Leu Gly Leu Val Gly Thr Thr Val Cys Ser Ala Phe Gln  
120 125 130 135

cat ctt ggt tgg gtt aaa agt ggc ttg ggc agt gga ccc aaa tgc tgc 544  
His Leu Gly Trp Val Lys Ser Gly Leu Gly Ser Gly Pro Lys Cys Cys  
140 145 150

cat taaagaatta taggggttta aaaactctca ttcatttta atgacttacc 597  
His

tttatttcca gttacatttt ttttctaaat ataataaaaa cttacctggc atcagcctca 657  
662

tacct

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aagcggttgcg ctcccggagg cgtccgcagc tgctggctgc tcatttgccg gtgaccggag 120  
gctcggggcc agc atg gcc ccc acg ctg caa cag gcg tac cgg agg cgc 169  
Met Ala Pro Thr Leu Gln Gln Ala Tyr Arg Arg Arg  
1 5 10

tgg tgg atg gcc tgc acg gct gtg ctg gag aac ctc ttc ttc tct gct 217  
Trp Trp Met Ala Cys Thr Ala Val Leu Glu Asn Leu Phe Phe Ser Ala  
15 20 25

gta ctc ctg ggc tgg ggc tcc ctg ttg atc att ctg aag aac gag ggc 265  
Val Leu Leu Gly Trp Gly Ser Leu Leu Ile Ile Leu Lys Asn Glu Gly  
30 35 40

ttc tat tcc agc acg tgc cca gct gag agc agc acc aac acc acc cag 313  
Phe Tyr Ser Ser Thr Cys Pro Ala Glu Ser Ser Thr Asn Thr Thr Gln  
45 50 55 60

gat gag cag cgc agg tgg cca ggc tgt gac cag cag gac gag atg ctc 361  
Asp Glu Gln Arg Trp Pro Gly Cys Asp Gln Gln Asp Glu Met Leu  
65 70 75

aac ctg ggc ttc acc att ggt tcc ttc gtg ctc agc gcc acc acc ctg 409  
Asn Leu Gly Phe Thr Ile Gly Ser Phe Val Leu Ser Ala Thr Thr Leu  
80 85 90

cca ctg ggg atc ctc atg gac cgc ttt ggc ccc cga ccc gtg cgg ctg 457  
Pro Leu Gly Ile Leu Met Asp Arg Phe Gly Pro Arg Pro Val Arg Leu  
95 100 105

gtt ggc agt gcc tgc ttc act gcg tcc tgc acc ctc atg gcc ctg gcc 505  
Val Gly Ser Ala Cys Phe Thr Ala Ser Cys Thr Leu Met Ala Leu Ala  
110 115 120

tcc cgg gac gtg gaa gct ctg tct ccg ttg ata ttc ctg gcg ctg tcc 553  
Ser Arg Asp Val Glu Ala Leu Ser Pro Leu Ile Phe Leu Ala Leu Ser  
125 130 135 140

ctg aat ggc ttt ggt ggc atc tgc cta acg ttc act tca ctc acg ctg 601  
Leu Asn Gly Phe Gly Gly Ile Cys Leu Thr Phe Thr Ser Leu Thr Leu  
145 150 155

ccc aac atg ttt ggg aac ctg cgc tcc acg tta atg gcc ctc atg att 649  
Pro Asn Met Phe Gly Asn Leu Arg Ser Thr Leu Met Ala Leu Met Ile  
160 165 170

ggc tct tac gcc tct tct gcc att acg ttc cca gga atc aag ctg atc 697  
Gly Ser Tyr Ala Ser Ser Ala Ile Thr Phe Pro Gly Ile Lys Leu Ile  
175 180 185

tac gat gcc ggt gtg gcc ttc gtg gtc atc atg ttc acc tgg tct ggc 745  
Tyr Asp Ala Gly Val Ala Phe Val Val Ile Met Phe Thr Trp Ser Gly  
190 195 200

ctg gcc tgc ctt atc ttt ctg aac tgc acc ctc aac tgg ccc atc gaa 793  
Leu Ala Cys Leu Ile Phe Leu Asn Cys Thr Leu Asn Trp Pro Ile Glu  
205 210 215 220

gcc ttt cct gcc cct gag gaa gtc aat tac acg aag aag atc aag ctg 841  
Ala Phe Pro Ala Pro Glu Glu Val Asn Tyr Thr Lys Lys Ile Lys Leu  
225 230 235

agt ggg ctg gcc ctg gac cac aag gtg aca ggt gac ctc ttc tac acc 889  
Ser Gly Leu Ala Leu Asp His Lys Val Thr Gly Asp Leu Phe Tyr Thr  
240 245 250

cat gtg acc acc atg ggc cag agg ctc agc cag aag gcc ccc agc ctg 937  
His Val Thr Thr Met Gly Gln Arg Leu Ser Gln Lys Ala Pro Ser Leu  
255 260 265

gag gac ggt tgc gat gcc ttc atg tca ccc cag gat gtt cgg gcc acc 985  
Glu Asp Gly Ser Asp Ala Phe Met Ser Pro Gln Asp Val Arg Gly Thr  
270 275 280

tca gaa aac ctt cct gag agg tct gtc ccc tta cgc aag agc ctc tgc 1033  
Ser Glu Asn Leu Pro Glu Arg Ser Val Pro Leu Arg Lys Ser Leu Cys  
285 290 295 300

tcc ccc act ttc ctg tgg agc ctc ctc acc atg ggc atg acc cag ctg 1081  
Ser Pro Thr Phe Leu Trp Ser Leu Leu Thr Met Gly Met Thr Gln Leu  
305 310 315

cgg atc atc ttc tac atg gct gct gtg aac aag atg ctg gag tac ctt 1129

Arg Ile Ile Phe Tyr Met Ala Ala Val Asn Lys Met Leu Glu Tyr Leu  
320 325 330

gtg act ggt ggc cag gag cat gag aca aat gaa cag caa caa aag gtg 1177  
Val Thr Gly Gly Gln Glu His Glu Thr Asn Glu Gln Gln Lys Val  
335 340 345

gca gag aca gtt ggg ttc tac tcc tcc gtc ttc ggg gcc atg cag ctg 1225  
Ala Glu Thr Val Gly Phe Tyr Ser Ser Val Phe Gly Ala Met Gln Leu  
350 355 360

ttg tgc ctt ctc acc tgc ccc ctc att ggc tac atc atg gac tgg cgg 1273  
Leu Cys Leu Leu Thr Cys Pro Leu Ile Gly Tyr Ile Met Asp Trp Arg  
365 370 375 380

atc aag gac tgc gtg gac gcc cca act cag ggc act gtc ctc gga gat 1321  
Ile Lys Asp Cys Val Asp Ala Pro Thr Gln Gly Thr Val Leu Gly Asp  
385 390 395

gcc agg gac ggg gtt gct acc aaa tcc atc aga cca cgc tac tgc aag 1369  
Ala Arg Asp Gly Val Ala Thr Lys Ser Ile Arg Pro Arg Tyr Cys Lys  
400 405 410

atc caa aag ctc acc aat gcc atc agt gcc ttc acc ctg acc aac ctg 1417  
Ile Gln Lys Leu Thr Asn Ala Ile Ser Ala Phe Thr Leu Thr Asn Leu  
415 420 425

ctg ctt gtg ggt ttt ggc atc acc tgt ctc atc aac aac tta cac ctc 1465  
Leu Leu Val Gly Phe Gly Ile Thr Cys Leu Ile Asn Asn Leu His Leu  
430 435 440

cag ttt gtg acc ttt gtc ctg cac acc att gtt cga ggt ttc ttc cac 1513  
Gln Phe Val Thr Phe Val Leu His Thr Ile Val Arg Gly Phe Phe His  
445 450 455 460

tca gcc tgt ggg agt ctc tat gct gca gtg ttc cca tcc aac cac ttt 1561  
Ser Ala Cys Gly Ser Leu Tyr Ala Ala Val Phe Pro Ser Asn His Phe  
465 470 475

ggg acg ctg aca ggc ctg cag tcc ctc atc agt gct gtg ttc gcc ttg 1609  
Gly Thr Leu Thr Gly Leu Gln Ser Leu Ile Ser Ala Val Phe Ala Leu  
480 485 490

ctt cag cag cca ctt ttc atg gcg atg gtg gga ccc ctg aaa gga gag 1657  
Leu Gln Gln Pro Leu Phe Met Ala Met Val Gly Pro Leu Lys Gly Glu  
495 500 505

ccc ttc tgg gtg aat ctg ggc ctc ctg cta ttc tca ctc ctg gga ttc 1705  
Pro Phe Trp Val Asn Leu Gly Leu Leu Leu Phe Ser Leu Leu Gly Phe  
510 515 520

ctg ttg cct tcc tac ctc ttc tat tac cgt gcc cgg ctc cag cag gag 1753  
Leu Leu Pro Ser Tyr Leu Phe Tyr Tyr Arg Ala Arg Leu Gln Gln Glu  
525 530 535 540

tac gcc gcc aat ggg atg ggc cca ctg aag gtg ctt agc ggc tct gag 1801  
Tyr Ala Ala Asn Gly Met Gly Pro Leu Lys Val Leu Ser Gly Ser Glu

545

550

555

gtg acc gca tagacttctc agaccaaggg acctggatga caggcaatca  
Val Thr Ala

1850

aggcctgagc aacccaaaagg agtgcccat atggcttttc tacctgtaac atgcacatag 1910  
agccatggcc gtagatttat aaataccaag agaagtctta tttttgtaaa gactgcaaaa 1970  
aggaggaaaa aaaaaccttc aaaaacgccc cctaagtcaa cgctccattg actgaagaca 2030  
gtccctatcc tagaggggtt gaggcttctt cctccttggg ttggaggaga ccagggtgcc 2090  
tcttatctcc ttctagcggg ctgcctcctg gtacctcttg gggggatcgg caaacaggct 2150  
accctgagg tcccatgtgc catgagtgtg cacacatgca tgtgtctgtg tatgtgtgaa 2210  
tgtgagagag acacagccct cctttcagaa ggaaaggggc ctgaggtgcc agctgtgtcc 2270  
tgggttaggg gttgggggtc ggccccttcc agggccagga gggcagggtc cctctctggt 2330  
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<220>  
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<222> (11)..(1000)

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Met Glu Gly Ala Pro Pro Gly Ser Leu Ala Leu Arg Leu  
1 5 10

ctg ctg ttc gtg gcg cta ccc gcc tcc ggc tgg ctg acg acg ggc gcc 97  
Leu Leu Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala  
15 20 25

ccc gag ccg ccg ccg ctg tcc gga gcc cca cag gac ggc atc aga att 145  
Pro Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile  
30 35 40 45

aat gta act aca ctg aaa gat gat ggg gac ata tct aaa cag cag gtt 193  
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln Val  
50 55 60

gtt ctt aac ata acc tat gag agt gga cag gtg tat gta aat gac tta 241  
Val Leu Asn Ile Thr Tyr Glu Ser Gly Gln Val Tyr Val Asn Asp Leu  
65 70 75

cct gta aat agt ggt gta acc cga ata agc tgt cag act ttg ata gtg 289  
Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr Leu Ile Val  
80 85 90



aag aat gaa aat ctt gaa aat ttg gag gaa aaa gaa tat ttt gga att 337  
Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu Tyr Phe Gly Ile  
95 100 105

gtc agt gta agg att tta gtt cat gag tgg cct atg aca tct ggt tcc 385  
Val Ser Val Arg Ile Leu Val His Glu Trp Pro Met Thr Ser Gly Ser  
110 115 120 125

agt ttg caa cta att gtc att caa gaa gag gta gta gag att gat gga 433  
Ser Leu Gln Leu Ile Val Ile Gln Glu Glu Val Val Glu Ile Asp Gly  
130 135 140

aaa caa gtt cag caa aag gat gtc act gaa att gat att tta gtt aag 481  
Lys Gln Val Gln Gln Lys Asp Val Thr Glu Ile Asp Ile Leu Val Lys  
145 150 155

aac cgg gga gta ctc aga cat tca aac tat acc ctc cct ttg gaa gaa 529  
Asn Arg Gly Val Leu Arg His Ser Asn Tyr Thr Leu Pro Leu Glu Glu  
160 165 170

agc atg ctc tac tct att tct cga gac agt gac att tta ttt acc ctt 577  
Ser Met Leu Tyr Ser Ile Ser Arg Asp Ser Asp Ile Leu Phe Thr Leu  
175 180 185

cct aac ctc tcc aaa aaa gaa agt gtt agt tca ctg caa acc act agc 625  
Pro Asn Leu Ser Lys Lys Glu Ser Val Ser Ser Leu Gln Thr Thr Ser  
190 195 200 205

cag tat ctt atc agg aat gtg gaa acc act gta gat gaa gat gtt tta 673  
Gln Tyr Leu Ile Arg Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu  
210 215 220

cct ggc aag tta cct gaa act cct ctc aga gca gag ccg cca tct tca 721  
Pro Gly Lys Leu Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser  
225 230 235

tat aag gta atg tgt cag tgg atg gaa aag ttt aga aaa gat ctg tgt 769  
Tyr Lys Val Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys  
240 245 250

agg ttc tgg agc aac gtt ttc cca gta ttc ttt cag ttt ttg aac atc 817  
Arg Phe Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile  
255 260 265

atg gtg gtt gga att aca gga gca gct gtg gta ata acc atc tta aag 865  
Met Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys  
270 275 280 285

gtg ttt ttc cca gtt tct gaa tac aaa gga att ctt cag ttg gat aaa 913  
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp Lys  
290 295 300

gtg gac gtc ata cct gtg aca gct atc aac tta tat cca gat ggt cca 961  
Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp Gly Pro  
305 310 315

gag aaa aga gct gaa aac ctt gaa gat aaa aca tgt att taaaacgcca 1010  
Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile  
320 325 330  
tctcatatca tggactccga agtagcctgt tgccctccaaa ttgcccactt gaataataatt 1070  
ttcttttaaat cgttaagaat cagtttatac actagagaaa ttgctaaact ctaagactgc 1130  
ctgaaaattg acctttacag tgccaagtta aagtttacct tattctcggc cgggtgcagt 1190  
ggctcatgcc tgtaatccca ggactttggg aggccaatgc gggcggatca cgaggtcaga 1250  
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1316  
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<400> 73  
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ccgtttgagc tcggtatcct agtgcacacg ccttgcaagc gacggcgcc atg agt ctg 118  
Met Ser Leu  
1

act tcc agt tcc agc gta cga gtt gaa tgg atc gca gca gtt acc att 166  
Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr Ile  
5 10 15

gct gct ggg aca gct gca att ggt tat cta gct tac aaa aga ttt tat 214  
Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe Tyr  
20 25 30 35

gtt aaa gat cat cga aat aaa gct atg ata aac ctt cac atc cag aaa 262  
Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln Lys  
40 45 50

gac aac ccc aag ata gta cat gct ttt gac atg gag gat ttg gga gat 310  
Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Leu Gly Asp  
55 60 65

aaa gct gtg tac tgc cgt tgt tgg agg tcc aaa aag ttc cca ttc tgt 358  
Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe Cys  
70 75 80

gat ggg gct cac aca aaa cat aac gaa gag act gga gac aat gtg ggc 406  
Asp Gly Ala His Thr Lys His Asn Glu Glu Thr Gly Asp Asn Val Gly  
85 90 95

cct ctg atc atc aag aaa gaa act taaatggaca cttttgatgc 453  
Pro Leu Ile Ile Lys Lys Lys Glu Thr  
100 105  
tgcaaatcag cttgtcgtga agttacctga ttgtttaatt agaatagacta ccacctctgt 513  
ctgattcacc ttcgctggat tctaaatgtg gtatattgca aactgcagct ttcacattta 573  
tggcatttgt cttgttgaaa catcgtgggt cacatttggt taaacaaaaa aaaaaaaaaa 633  
aaggaaaaac caacctcatg gcctgtgggt tattttgggtc ttgtaaggat ccatttcttt 693  
aaaatactga catatagagt tgtaccttat atagaatata gttgtatctt gaagtcaaca 753  
tattaaatta ttctcaaaat tatgtatttg cagattgtac ttgtaagttt caaagaaaaa 813  
ttaccatctt ttcattatga cctggaaact aaataggatg tgattcagct acattaattt 873  
cttaatacaa tctaggaaag 893

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<212> DNA  
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<220>  
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<400> 74  
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gtgagctctc ctggggcgtg gttgttcgtg atccttgcat ctgttactta gggtaaggc 180  
ttgggtcttg ccccgacagc ccttgggacg acccgcccc agcgcagct atg aac ctg 238  
Met Asn Leu  
1

gag cga gtg tcc aat gag gag aaa ttg aac ctg tgc cgg aag tac tac 286  
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr  
5 10 15

ctg ggg ggg ttt gct ttc ctg cct ttt ctc tgg ttg gtc aac atc ttc 334  
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe  
20 25 30 35

tgg ttc ttc cga gag gcc ttc ctt gtc cca gcc tac aca gaa cag agc 382  
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser  
40 45 50

caa atc aaa ggc tat gtc tgg cgc tca gct gtg ggc ttc ctc ttc tgg 430  
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp  
55 60 65

gtg ata gtg ctc acc tcc tgg atc acc atc ttc cag atc tac cgg ccc 478  
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro  
70 75 80

cgc tgg ggt gcc ctt ggg gac tac ctc tcc ttc acc ata ccc ctg ggc 526  
Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile Pro Leu Gly  
85 90 95

acc ccc tgacaacttc tgcacatact ggggacctgc ttattctccc aggacaggct 582  
Thr Pro  
100

ccttaaagca gaggagcctg tcttgggagc cccttctcaa actcctaaga cttgttttca 642  
tgtccacgt tctctgctga catcccccaa taaaggaccc taactttc 690

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<212> DNA  
<213> Homo sapiens

<220>  
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<400> 75  
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tctgggggag cgcgccagga ggctcctcag gccgacccca gacctgggt gccagg 117

atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 165  
Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala  
1 5 10 15

atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 213  
Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro  
20 25 30

acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 261  
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala  
35 40 45

tgg ccc act cca ccc acc cgc cca gcc ccg gcc ccg tgc cat gcc aac 309  
Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn  
50 55 60

acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt 357  
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val  
65 70 75 80

cag aac ttc ctc ctg tac aga cac tgc cgc cac ttt ccc ctg ctg cag 405  
Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln  
85 90 95

gac gtg ccc ccc tct aag tgc gcg cag ccg gtc ttc ctg ctg ctg gtg 453  
Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val

100	105	110	
atc aag tcc tcc cct agc aac	tat gtg cgc cgc gag	ctg ctg cgg cgc	501
Ile Lys Ser Ser Pro Ser Asn	Tyr Val Arg Arg Glu	Leu Leu Arg Arg	
115	120	125	
acg tgg ggc cgc gag cgc aag	gta cgg ggt ttg cag	ctg cgc ctc ctc	549
Thr Trp Gly Arg Glu Arg Lys	Val Arg Gly Leu Gln	Leu Arg Leu Leu	
130	135	140	
ttc ctg gtg ggc aca gcc tcc aac	cgc gag gcc cgc aag gtc aac		597
Phe Leu Val Gly Thr Ala Ser Asn	Pro His Glu Ala Arg Lys Val Asn		
145	150	155	160
cgg ctg ctg gag ctg gag gca cag	act cac gga gac atc ctg cag tgg		645
Arg Leu Leu Glu Leu Glu Ala Gln	Thr His Gly Asp Ile Leu Gln Trp		
165	170	175	
gac ttc cac gac tcc ttc ttc aac	ctc acg ctc aag cag gtc ctg ttc		693
Asp Phe His Asp Ser Phe Phe Asn	Leu Thr Leu Lys Gln Val Leu Phe		
180	185	190	
tta cag tgg cag gag aca agg tgc	gcc aac gcc agc ttc gtg ctc aac		741
Leu Gln Trp Gln Glu Thr Arg Cys	Ala Asn Ala Ser Phe Val Leu Asn		
195	200	205	
ggg gat gat gac gtc ttt gca cac	aca gac aac atg gtc ttc tac ctg		789
Gly Asp Asp Asp Val Phe Ala His	Thr Asp Asn Met Val Phe Tyr Leu		
210	215	220	
cag gac cat gac cct ggc cgc cac	ctc ttc gtg ggg caa ctg atc caa		837
Gln Asp His Asp Pro Gly Arg His	Leu Phe Val Gly Gln Leu Ile Gln		
225	230	235	240
aac gtg ggc ccc atc cgg gct ttt	tgg agc aag tac tat gtg cca gag		885
Asn Val Gly Pro Ile Arg Ala Phe	Trp Ser Lys Tyr Tyr Val Pro Glu		
245	250	255	
gtg gtg act cag aat gag cgg tac	cca ccc tat tgt ggg ggt ggt ggc		933
Val Val Thr Gln Asn Glu Arg Tyr	Pro Pro Tyr Cys Gly Gly Gly Gly		
260	265	270	
ttc ttg ctg tcc cgc ttc acg gcc	gct gcc ctg cgc cgt gct gcc cat		981
Phe Leu Leu Ser Arg Phe Thr Ala	Ala Ala Leu Arg Arg Ala Ala His		
275	280	285	
gtc ttg gac atc ttc ccc att gat	gat gtc ttc ctg ggt atg tgt ctg		1029
Val Leu Asp Ile Phe Pro Ile Asp	Asp Asp Val Phe Leu Gly Met Cys Leu		
290	295	300	
gag ctt gag gga ctg aag cct gcc	tcc cac agc ggc atc cgc acg tct		1077
Glu Leu Glu Gly Leu Lys Pro Ala	Ser His Ser Gly Ile Arg Thr Ser		
305	310	315	320
ggc gtg cgg gct cca tgc caa cac	ctg tcc tcc ttt gac ccc tgc ttc		1125
Gly Val Arg Ala Pro Ser Gln His	Leu Ser Ser Phe Asp Pro Cys Phe		
325	330	335	

tac cga gac ctg ctg ctg gtg cac cgc ttc cta cct tat gag atg ctg 1173  
Tyr Arg Asp Leu Leu Leu Val His Arg Phe Leu Pro Tyr Glu Met Leu  
340 345 350

ctc atg tgg gat gcg ctg aac cag ccc aac ctc acc tgc ggc aat cag 1221  
Leu Met Trp Asp Ala Leu Asn Gln Pro Asn Leu Thr Cys Gly Asn Gln  
355 360 365

aca cag atc tac tgagtcagca tcagggtccc cagcctctgg gctcctgttt 1273  
Thr Gln Ile Tyr  
370

ccataggaag gggcgacacc ttctctccag gaagctgaga cctttgtggt ctgagcataa 1333  
gggagtgccca gggaagggtt gaggtttgat gagtgaatat tctggctggc gaactcctac 1393  
acatccttca aaaccacct ggtactgttc cagcatcttc cctggatggc tggaggaact 1453  
ccagaaaata tccatcttct ttttgtggct gctaattggca gaagtgcctg tgctagagtt 1513  
ccaactgtgg atgcatccgt cccgtttgag tcaaagtctt acttccctgc tctcacctac 1573  
tcacagacgg gatgctaagc agtgcacctg cagtgggtta atggcagata agctccgtct 1633  
gcagttccag gccagccaga aactcctgtg tccacataga gctgacgtga gaaatatctt 1693  
tcagcccagg agagaggggt cctgatctta accctttcct gggctctcaga caactcagaa 1753  
ggttgggggg ataccagaga ggtggtggaa taggaccgcc cctccttac ttgtgggac 1813  
aaatgctgta atggtggagg tgtgggcaga ggagggaggc aagtgtcctt tgaaagtgt 1873  
gagagctcag agtttctggg gtcctcatta ggagccccc tccctgtgtt cccaagaat 1933  
tcagagaaca gcaactggggc tggaatgatc tttaattgggc ccaaggccaa caggcatatg 1993  
cctcactact gcctggagaa gggagagatt caggctcctcc agcagcctcc ctcacccagt 2053  
atgttttaca gattacgggg ggaccgggtg agccagtgc cccctgcagc cccagcttc 2113  
aggcctcagt gtctgccagt caagcttcac aggcattgtg atggggcagc cttggggaat 2173  
ataaaatttt gtg 2186

<210> 76  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: restriction  
enzyme cleavage sequence

<400> 76  
gaattccaca gatcccggt cagctgggat atccctctc tcct

44

<210> 77  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: fusion protein  
start site

<400> 77  
Pro Ser Ser Pro  
1

<210> 78  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: oligo DNA  
linker

<400> 78  
gatcccggt cacgtgggat

20

<210> 79  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: oligo DNA  
linker

<400> 79  
atcccacgtg acccgg

16

<210> 80  
<211> 213  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 80  
Met Asn Lys Glu Ser Lys Asp Asp Asp Met Ser Leu Gly Lys Phe Ser  
1 5 10 15

Phe Ser His Phe Leu Tyr Tyr Leu Val Leu Ile Val Val Ile Val Tyr  
20 25 30

Gly Leu Tyr Lys Leu Phe Thr Gly His Gly Ser Asp Ile Asn Phe Gly  
35 40 45

Lys Phe Leu Leu Arg Thr Ser Pro Tyr Met Trp Ala Asn Leu Gly Ile

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<210> 81
<211> 394
<212> PRT
<213> Rattus sp.
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Phe Gln Asp Pro Gly Ser Pro Gln His Gly Asn Tyr Gln Glu Glu Gly  
100 105 110

Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ser Val Asn Trp Asp  
115 120 125

Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val Leu Thr  
130 135 140

Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ala Ile Phe Thr Phe Val  
145 150 155 160

Gly Glu Val Lys Gly Phe Val Arg Ala Asn Val Trp Thr Tyr Tyr Val  
165 170 175

Ser Tyr Ala Ile Phe Phe Ile Ser Leu Ile Val Leu Ser Cys Cys Gly  
180 185 190

Asp Phe Arg Lys Lys His Pro Trp Asn Leu Val Ala Leu Ser Ile Leu  
195 200 205

Thr Ile Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe Tyr Asn  
210 215 220

Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val Cys Phe  
225 230 235 240

Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys  
245 250 255

Met Gly Val Leu Leu Val Ser Val Val Val Leu Phe Ile Phe Ala Ile  
260 265 270

Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser  
275 280 285

Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr Gln Leu  
290 295 300

Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe  
305 310 315 320

Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile  
325 330 335

Leu Thr Ile Ile Gly Arg Ser Gln Gly Ile Gly Gln Ala Pro Ala Gln  
340 345 350

Val Ala Trp Trp Ala Gln Thr His Ala Pro Ala Met Thr Leu Pro Ser  
355 360 365

Val Leu Pro Pro Leu Trp Phe Pro Ala Met Ala Trp Ser Arg Gly Ser  
370 375 380

Pro Ser Arg Pro Arg Val Cys Thr Leu Gln  
385 390

<210> 82  
<211> 406  
<212> PRT  
<213> Bovine Sp.

<400> 82  
Val Leu Pro Gln Cys Asn Asp Phe Leu Ser Gln Pro Ala Gly Ser Ala 15  
1 5 10  
Ala Ser Glu Glu Ser Ser Pro Tyr Cys Ser Asp Ser Arg Gln Leu Arg 30  
20 25  
Leu Val Asp Gly Gly Gly Pro Cys Gly Gly Arg Val Glu Ile Leu Asp 45  
35 40  
Gln Gly Ser Trp Gly Thr Ile Cys Asp Asp Asp Trp Asp Leu Asp Asp 60  
50 55  
Ala Arg Val Val Cys Arg Gln Leu Gly Cys Gly Glu Ala Leu Asn Ala 80  
65 70 75  
Thr Gly Ser Ala His Phe Gly Ala Gly Ser Gly Pro Ile Trp Leu Asp 95  
85 90  
Asp Leu Asn Cys Thr Gly Lys Glu Ser His Val Trp Arg Cys Pro Ser 110  
100 105  
Arg Gly Trp Gly Arg His Asp Cys Arg His Lys Glu Asp Ala Gly Val 125  
115 120  
Ile Cys Ser Glu Phe Leu Ala Leu Arg Met Val Ser Glu Asp Gln Gln 140  
130 135  
Cys Ala Gly Trp Leu Glu Val Phe Tyr Asn Gly Thr Trp Gly Ser Val 160  
145 150 155  
Cys Arg Ser Pro Met Glu Asp Ile Thr Val Ser Val Ile Cys Arg Gln 175  
165 170  
Leu Gly Cys Gly Asp Ser Gly Ser Leu Asn Thr Ser Val Gly Leu Arg 190  
180 185  
Glu Gly Ser Arg Pro Arg Trp Val Asp Leu Ile Gln Cys Arg Lys Met 205  
195 200  
Asp Thr Ser Leu Trp Gln Cys Pro Ser Gly Pro Trp Lys Tyr Ser Ser 220  
210 215  
Cys Ser Pro Lys Glu Glu Ala Tyr Ile Ser Cys Glu Gly Arg Arg Pro 240  
225 230 235  
Lys Ser Cys Pro Thr Ala Ala Ala Cys Thr Asp Arg Glu Lys Leu Arg 255  
245 250  
Leu Arg Gly Gly Asp Ser Glu Cys Ser Gly Arg Val Glu Val Trp His 270  
260 265 270

Asn Gly Ser Trp Gly Thr Val Cys Asp Asp Ser Trp Ser Leu Ala Glu  
275 280 285

Ala Glu Val Val Cys Gln Gln Leu Gly Cys Gly Gln Ala Leu Glu Ala  
290 295 300

Val Arg Ser Ala Ala Phe Gly Pro Gly Asn Gly Ser Ile Trp Leu Asp  
305 310 315 320

Glu Val Gln Cys Gly Gly Arg Glu Ser Ser Leu Trp Asp Cys Val Ala  
325 330 335

Glu Pro Trp Gly Gln Ser Asp Cys Lys His Glu Glu Asp Ala Gly Val  
340 345 350

Arg Cys Ser Gly Val Arg Thr Thr Leu Pro Thr Thr Thr Ala Gly Thr  
355 360 365

Arg Thr Thr Ser Asn Ser Leu Pro Gly Ile Phe Ser Leu Pro Gly Val  
370 375 380

Leu Cys Leu Ile Leu Gly Ser Leu Leu Phe Leu Val Leu Val Ile Leu  
385 390 395 400

Val Thr Gln Leu Leu Arg  
405

<210> 83  
<211> 556  
<212> PRT  
<213> Mus sp.

<400> 83  
Met Pro Thr Val Asp Asp Val Leu Glu Gln Val Gly Glu Phe Gly Trp  
1 5 10 15

Phe Gln Lys Gln Ala Phe Leu Leu Leu Cys Leu Ile Ser Ala Ser Leu  
20 25 30

Ala Pro Ile Tyr Val Gly Ile Val Phe Leu Gly Phe Thr Pro Gly His  
35 40 45

Tyr Cys Gln Asn Pro Gly Val Ala Glu Leu Ser Gln Arg Cys Gly Trp  
50 55 60

Ser Gln Ala Glu Glu Leu Asn Tyr Thr Val Pro Gly Leu Gly Pro Ser  
65 70 75 80

Asp Glu Ala Ser Phe Leu Ser Gln Cys Met Arg Tyr Glu Val Asp Trp  
85 90 95

Asn Gln Ser Thr Leu Asp Cys Val Asp Pro Leu Ser Ser Leu Val Ala  
100 105 110

Asn Arg Ser Gln Leu Pro Leu Gln Pro Cys Glu His Gly Trp Val Tyr

115 120 125  
Asp Thr Pro Gly Ser Ser Ile Val Thr Glu Phe Asn Leu Val Cys Gly  
130 135 140  
Asp Ala Trp Lys Val Asp Leu Phe Gln Ser Cys Val Asn Leu Gly Phe  
145 150 155 160  
Phe Leu Gly Ser Leu Val Val Gly Tyr Ile Ala Asp Arg Phe Gly Arg  
165 170 175  
Lys Leu Cys Leu Leu Val Thr Thr Leu Val Thr Ser Val Ser Gly Val  
180 185 190  
Leu Thr Ala Val Ala Pro Asp Tyr Thr Ser Met Leu Leu Phe Arg Leu  
195 200 205  
Leu Gln Gly Met Val Ser Lys Gly Ser Trp Val Ser Gly Tyr Thr Leu  
210 215 220  
Ile Thr Glu Phe Val Gly Ser Gly Tyr Arg Arg Thr Thr Ala Ile Leu  
225 230 235 240  
Tyr Gln Met Ala Phe Thr Val Gly Leu Val Gly Leu Ala Gly Val Ala  
245 250 255  
Tyr Ala Ile Pro Asp Trp Arg Trp Leu Gln Leu Ala Val Ser Leu Pro  
260 265 270  
Thr Phe Leu Phe Leu Leu Tyr Tyr Trp Phe Val Pro Glu Ser Pro Arg  
275 280 285  
Trp Leu Leu Ser Gln Lys Arg Thr Thr Arg Ala Val Arg Ile Met Glu  
290 295 300  
Gln Ile Ala Gln Lys Asn Gly Lys Val Pro Pro Ala Asp Leu Lys Met  
305 310 315 320  
Leu Cys Leu Glu Glu Asp Ala Ser Glu Lys Arg Ser Pro Ser Phe Ala  
325 330 335  
Asp Leu Phe Arg Thr Pro Asn Leu Arg Lys His Thr Val Ile Leu Met  
340 345 350  
Tyr Leu Trp Phe Ser Cys Ala Val Leu Tyr Gln Gly Leu Ile Met His  
355 360 365  
Val Gly Ala Thr Gly Ala Asn Leu Tyr Leu Asp Phe Phe Tyr Ser Ser  
370 375 380  
Leu Val Glu Phe Pro Ala Ala Phe Ile Ile Leu Val Thr Ile Asp Arg  
385 390 395 400  
Ile Gly Arg Ile Tyr Pro Ile Ala Ala Ser Asn Leu Val Thr Gly Ala  
405 410 415  
Ala Cys Leu Leu Met Ile Phe Ile Pro His Glu Leu His Trp Leu Asn

420 425 430  
Val Thr Leu Ala Cys Leu Gly Arg Met Gly Ala Thr Ile Val Leu Gln  
435 440 445  
Met Val Cys Leu Val Asn Ala Glu Leu Tyr Pro Thr Phe Ile Arg Asn  
450 455 460  
Leu Gly Met Met Val Cys Ser Ala Leu Cys Asp Leu Gly Gly Ile Phe  
465 470 475 480  
Thr Pro Phe Met Val Phe Arg Leu Met Glu Val Trp Gln Ala Leu Pro  
485 490 495  
Leu Ile Leu Phe Gly Val Leu Gly Leu Thr Ala Gly Ala Met Thr Leu  
500 505 510  
Leu Leu Pro Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Ile Glu Glu  
515 520 525  
Ala Glu Asn Leu Gly Arg Arg Lys Ser Lys Ala Lys Glu Asn Thr Ile  
530 535 540  
Tyr Leu Gln Val Gln Thr Gly Lys Ser Ser Ser Thr  
545 550 555  
  
<210> 84  
<211> 202  
<212> PRT  
<213> Homo sapiens  
  
<400> 84  
Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser Leu Val Gly  
1 5 10 15  
Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr Phe Pro Asn  
20 25 30  
Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp  
35 40 45  
Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala  
50 55 60  
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly  
65 70 75 80  
His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala  
85 90 95  
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala  
100 105 110  
Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp  
115 120 125

Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser  
130 135 140

Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val  
145 150 155 160

Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu  
165 170 175

Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe  
180 185 190

Cys Cys Ser His Gln Gln Gln Tyr Asp Cys  
195 200

<210> 85  
<211> 214  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 85  
Met Ile Thr Ser Phe Leu Met Glu Lys Met Thr Val Ser Ser Asn Tyr  
1 5 10 15

Thr Ile Ala Leu Trp Ala Thr Phe Thr Ala Ile Ser Phe Ala Val Gly  
20 25 30

Tyr Gln Leu Gly Thr Ser Asn Ala Ser Ser Thr Lys Lys Ser Ser Ala  
35 40 45

Thr Leu Leu Arg Ser Lys Glu Met Lys Glu Gly Lys Leu His Asn Asp  
50 55 60

Thr Asp Glu Glu Glu Ser Glu Ser Glu Asp Glu Ser Asp Glu Asp Glu  
65 70 75 80

Asp Ile Glu Ser Thr Ser Leu Asn Asp Ile Pro Gly Glu Val Arg Met  
85 90 95

Ala Leu Val Ile Arg Gln Asp Leu Gly Met Thr Lys Gly Lys Ile Ala  
100 105 110

Ala Gln Cys Cys His Ala Ala Leu Ser Cys Phe Arg His Ile Ala Thr  
115 120 125

Asn Pro Ala Arg Ala Ser Tyr Asn Pro Ile Met Thr Gln Arg Trp Leu  
130 135 140

Asn Ala Gly Gln Ala Lys Ile Thr Leu Lys Cys Pro Asp Lys Phe Thr  
145 150 155 160

Met Asp Glu Leu Tyr Ala Lys Ala Ile Ser Leu Gly Val Asn Ala Ala  
165 170 175

Val Ile His Asp Ala Gly Arg Thr Gln Ile Ala Ala Gly Ser Ala Thr  
180 185 190

Val Leu Gly Leu Gly Pro Ala Pro Lys Ala Val Leu Asp Gln Ile Thr  
195 200 205

Gly Asp Leu Lys Leu Tyr  
210

<210> 86  
<211> 199  
<212> PRT  
<213> Homo sapiens

<400> 86  
Met Ser Ser Glu Asn Cys Phe Val Ala Glu Asn Ser Ser Leu His Pro  
1 5 10 15

Glu Ser Gly Gln Glu Asn Asp Ala Thr Ser Pro His Phe Ser Thr Arg  
20 25 30

His Glu Gly Ser Phe Gln Val Pro Val Leu Cys Ala Val Met Asn Val  
35 40 45

Val Phe Ile Thr Ile Leu Ile Ala Leu Ile Ala Leu Ser Val Gly  
50 55 60

Gln Tyr Asn Cys Pro Gly Gln Tyr Thr Phe Ser Met Pro Ser Asp Ser  
65 70 75 80

His Val Ser Ser Cys Ser Glu Asp Trp Val Gly Tyr Gln Arg Lys Cys  
85 90 95

Tyr Phe Ile Ser Thr Val Lys Arg Ser Trp Thr Ser Ala Gln Asn Ala  
100 105 110

Cys Ser Glu His Gly Ala Thr Leu Ala Val Ile Asp Ser Glu Lys Asp  
115 120 125

Met Asn Phe Leu Lys Arg Tyr Ala Gly Arg Glu Glu His Trp Val Gly  
130 135 140

Leu Lys Lys Glu Pro Gly His Pro Trp Lys Trp Ser Asn Gly Lys Glu  
145 150 155 160

Phe Asn Asn Trp Phe Asn Val Thr Gly Ser Asp Lys Cys Val Phe Leu  
165 170 175

Lys Asn Thr Glu Val Ser Ser Met Glu Cys Glu Lys Asn Leu Tyr Trp  
180 185 190

Ile Cys Asn Lys Pro Tyr Lys  
195

<210> 87  
<211> 214  
<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 87

Met Ile Lys Ser Thr Leu Ile Tyr Arg Glu Asp Gly Leu Pro Leu Cys  
1 5 10 15  
Thr Ser Val Asp Asn Glu Asn Asp Pro Ser Leu Phe Glu Gln Lys Gln  
20 25 30  
Lys Val Lys Ile Val Val Ser Arg Leu Thr Pro Gln Ser Ala Thr Glu  
35 40 45  
Ala Thr Leu Glu Ser Gly Ser Phe Glu Ile His Tyr Leu Lys Lys Ser  
50 55 60  
Met Val Tyr Tyr Phe Val Ile Cys Glu Ser Gly Tyr Pro Arg Asn Leu  
65 70 75 80  
Ala Phe Ser Tyr Leu Asn Asp Ile Ala Gln Glu Phe Glu His Ser Phe  
85 90 95  
Ala Asn Glu Tyr Pro Lys Pro Thr Val Arg Pro Tyr Gln Phe Val Asn  
100 105 110  
Phe Asp Asn Phe Leu Gln Met Thr Lys Lys Ser Tyr Ser Asp Lys Lys  
115 120 125  
Val Gln Asp Asn Leu Asp Gln Leu Asn Gln Glu Leu Val Gly Val Lys  
130 135 140  
Gln Ile Met Ser Lys Asn Ile Glu Asp Leu Leu Tyr Arg Gly Asp Ser  
145 150 155 160  
Leu Asp Lys Met Ser Asp Met Ser Ser Ser Leu Lys Glu Thr Ser Lys  
165 170 175  
Arg Tyr Arg Lys Ser Ala Gln Lys Ile Asn Phe Asp Leu Leu Ile Ser  
180 185 190  
Gln Tyr Ala Pro Ile Val Ile Val Ala Phe Phe Phe Val Phe Leu Phe  
195 200 205  
Trp Trp Ile Phe Leu Lys  
210

<210> 88

<211> 326

<212> PRT

<213> *Homo sapiens*

<400> 88

Met Ala Ser Val Cys Phe Ile Asn Ser Phe Ser Ala Val Leu Gln Gly  
1 5 10 15  
Ser Leu Phe Gly Gln Leu Gly Thr Met Pro Ser Thr Tyr Ser Thr Leu  
20 25 30



Phe Leu Ser Gly Gln Gly Leu Ala Gly Ile Phe Ala Ala Leu Ala Met  
35 40 45

Leu Leu Ser Met Ala Ser Gly Val Asp Ala Glu Thr Ser Ala Leu Gly  
50 55 60

Tyr Phe Ile Thr Pro Tyr Val Gly Ile Leu Met Ser Ile Val Cys Tyr  
65 70 75 80

Leu Ser Leu Pro His Leu Lys Phe Ala Arg Tyr Tyr Leu Ala Asn Lys  
85 90 95

Ser Ser Gln Ala Gln Ala Gln Glu Leu Glu Thr Lys Ala Glu Leu Leu  
100 105 110

Gln Ser Asp Glu Asn Gly Ile Pro Ser Ser Pro Gln Lys Val Ala Leu  
115 120 125

Thr Leu Asp Leu Asp Leu Glu Lys Glu Pro Glu Ser Glu Pro Asp Glu  
130 135 140

Pro Gln Lys Pro Gly Lys Pro Ser Val Phe Thr Val Phe Gln Lys Ile  
145 150 155 160

Trp Leu Thr Ala Leu Cys Leu Val Leu Val Phe Thr Val Thr Leu Ser  
165 170 175

Val Phe Pro Ala Ile Thr Ala Met Val Thr Ser Ser Thr Ser Pro Gly  
180 185 190

Lys Trp Ser Gln Phe Phe Asn Pro Ile Cys Cys Phe Leu Leu Phe Asn  
195 200 205

Ile Met Asp Trp Leu Gly Arg Ser Leu Thr Ser Tyr Phe Leu Trp Pro  
210 215 220

Asp Glu Asp Ser Arg Leu Leu Pro Leu Leu Val Cys Leu Arg Phe Leu  
225 230 235 240

Phe Val Pro Leu Phe Met Leu Cys His Val Pro Gln Arg Ser Arg Leu  
245 250 255

Pro Ile Leu Phe Pro Gln Asp Ala Tyr Phe Ile Thr Phe Met Leu Leu  
260 265 270

Phe Ala Val Ser Asn Gly Tyr Leu Val Ser Leu Thr Met Cys Leu Ala  
275 280 285

Pro Arg Gln Val Leu Pro His Glu Arg Glu Val Ala Gly Ala Leu Met  
290 295 300

Thr Phe Phe Leu Ala Leu Gly Leu Ser Cys Gly Ala Ser Leu Ser Phe  
305 310 315 320

Leu Phe Lys Ala Leu Leu  
325

<210> 89  
<211> 146  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 89  
Met Val Leu Pro Ile Ile Ile Gly Leu Gly Val Thr Met Val Ala Leu  
1 5 10 15  
Ser Val Lys Ser Gly Leu Asn Ala Trp Thr Val Tyr Lys Thr Leu Ser  
20 25 30  
Pro Leu Thr Ile Ala Lys Leu Asn Asn Ile Arg Ile Glu Asn Pro Thr  
35 40 45  
Ala Gly Tyr Arg Asp Ala Leu Lys Phe Lys Ser Ser Leu Ile Asp Glu  
50 55 60  
Glu Leu Lys Asn Arg Leu Asn Gln Tyr Gln Gly Gly Phe Ala Pro Arg  
65 70 75 80  
Met Thr Glu Pro Glu Ala Leu Leu Ile Leu Asp Ile Ser Ala Arg Glu  
85 90 95  
Ile Asn His Leu Asp Glu Lys Leu Leu Lys Lys Lys His Arg Lys Ala  
100 105 110  
Met Val Arg Asn His Pro Asp Arg Gly Gly Ser Pro Tyr Met Ala Ala  
115 120 125  
Lys Ile Asn Glu Ala Lys Glu Val Leu Glu Arg Ser Val Leu Leu Arg  
130 135 140  
Lys Arg  
145

<210> 90  
<211> 325  
<212> PRT  
<213> *Drosophila* sp.

<400> 90  
Met Gln Ser Lys His Arg Lys Leu Leu Leu Arg Cys Leu Leu Val Leu  
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Pro Leu Ile Leu Leu Val Asp Tyr Cys Gly Leu Leu Thr His Leu His  
20 25 30  
Glu Leu Asn Phe Glu Arg His Phe His Tyr Pro Leu Asn Asp Asp Thr  
35 40 45  
Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg  
50 55 60

Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu 80  
65 70 75  
Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala 95  
85 90  
Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu 110  
100 105  
Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val 125  
115 120  
Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr 140  
130 135  
Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp 160  
145 150  
Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp 175  
165 170  
Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly 190  
180 185  
Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln 205  
195 200  
Thr Ser Pro Leu Arg His Lys Phe Ser Lys Trp Tyr Val Ser Leu Glu 220  
210 215  
Glu Tyr Pro Phe Asp Arg Trp Pro Pro Tyr Val Thr Ala Gly Ala Phe 240  
225 230 235  
Ile Leu Ser Gln Lys Ala Leu Arg Gln Leu Tyr Ala Ala Ser Val His 255  
245 250  
Leu Pro Leu Phe Arg Phe Asp Asp Val Tyr Leu Gly Ile Val Ala Leu 270  
260 265  
Lys Ala Gly Ile Ser Leu Gln His Cys Asp Asp Phe Arg Phe His Arg 285  
275 280  
Pro Ala Tyr Lys Gly Pro Asp Ser Tyr Ser Ser Val Ile Ala Ser His 300  
290 295  
Glu Phe Gly Asp Pro Glu Glu Met Thr Arg Val Trp Asn Glu Cys Arg 320  
305 310 315  
Ser Ala Asn Tyr Ala 325

<210> 91  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Combined DNA/RNA Molecule:  
Nucleotides at positions 12-14 are RNA

<220>

<223> Description of Artificial Sequence: DNA/RNA  
chimeric oligonucleotide

<400> 91

ggggaattcg agga

14